

QY 298 VKLISYDC-VR-S---ELE-SY-----RCPGFVVRROSLVILKDYCRPRPLYEPHYV 342

Db 361 RAHEKRLADLVLSIDSTPKOSKSDMWMTDFRPTASLKQVSLMDLADNLRPNVNSG 420

QY 343 RAHEKRLADLVLSIDSTPKOSKSDMWMTDFRPTASLKQVSLMDLADNLRPNVNSG 402

Db 421 FDEPADVMYRIEFSYVYGLTLTASKSTTKYNAOPAKNKKMYFDLYMKDMPSSAVLS 480

QY 403 FDEPADVMYRIEFSYVYGLTLTASKSTTKYNAOPAKNKKMYFDLYMKDMPSSAVLS 462

Db 481 IRLVGLKVKIKSEEEVGVNNSLMDWDELROGQFLFHLMAPEPTANRSRIGENGARIG 540

QY 463 IRLVGLKVKIKSEEEVGVNNSLMDWDELROGQFLFHLMAPEPTANRSRIGENGARIG 522

Db 541 TNAAVTIEISSYGRVRRPSCQGYTYLVKHSRTWETLINMGDDYESCIRDPGYKRLQML 600

QY 523 TNAAVTIEISSYGRVRRPSCQGYTYLVKHSRTWETLINMGDDYESCIRDPGYKRLQML 582

Db 601 VKHHSGLVLEDEORHVMWRRYIQOKOEPDLILVSELAFTWDRENSELYVMLEKKK 660

QY 583 VKHHSGLVLEDEORHVMWRRYIQOKOEPDLILVSELAFTWDRENSELYVMLEKKK 642

Db 661 PPSVAAALTLGKRCCTDRYIRKFAVEKLENEOLSPYTFHFLPLQALKYEPRAOSEVM 720

QY 643 PPSVAAALTLGKRCCTDRYIRKFAVEKLENEOLSPYTFHFLPLQALKYEPRAOSEVM 702

Db 721 MLTRALCDYRIGHRLFMILRAELARLRCDCSESEYRISILMEAYILRGNEEHKIIIR 780

QY 703 MLTRALCDYRIGHRLFMILRAELARLRCDCSESEYRISILMEAYILRGNEEHKIIIR 762

Db 761 QVDVDELTRISTLVKGMKDYATMKLDELRSISHKMNMDSPIDPYKKGEMIIDKAI 840

QY 763 QVDVDELTRISTLVKGMKDYATMKLDELRSISHKMNMDSPIDPYKKGEMIIDKAI 822

Db 841 VLSGAKRPLMLMKKNKPSDLHPCAMIFKNGDILRODMVLYOLEVMDNIMKRAAND 900

QY 823 VLSGAKRPLMLMKKNKPSDLHPCAMIFKNGDILRODMVLYOLEVMDNIMKRAAND 882

Db 901 CCLNPAVALPMGEMIGILIEVENCCTIFELIYGTGFMNTAVRSIDPSFNKKIRKOCGIE 960

QY 883 CCLNPAVALPMGEMIGILIEVENCCTIFELIYGTGFMNTAVRSIDPSFNKKIRKOCGIE 942

Db 961 DEKKSCKDSTNPIEKKIDTQAMKKTIESYDRFLYSCVGSVATYIMGIDRHSNIM 1020

QY 943 DEKKSCKDSTNPIEKKIDTQAMKKTIESYDRFLYSCVGSVATYIMGIDRHSNIM 1002

Db 1021 LTEDKRYHIDGHILGKTKLGIDORDOPILTEHEFTVIRSGKSVDSGNSHELOKFT 1080

QY 1003 LTEDKRYHIDGHILGKTKLGIDORDOPILTEHEFTVIRSGKSVDSGNSHELOKFT 1062

Db 1081 LCEVAYEVMMNNRDLFVSLFTLMLGMELEPSTKADLDHLKTLFCNGESKEARKEAFAG 1140

QY 1063 LCEVAYEVMMNNRDLFVSLFTLMLGMELEPSTKADLDHLKTLFCNGESKEARKEAFAG 1122

Db 1141 IYEEAFNGSWSKTITWMLFRAVKHY 1164

QY 1123 IYEEAFNGSWSKTITWMLFRAVKHY 1146

RESULT 2

ENTRY 138110 #type complete

TITLE 1-phosphatidylinositol 3-kinase (EC 2.7.1.137) - human

ORGANISM #formal_name Homo sapiens #common_name man

DATE 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 21-Nov-1997

ACCESSIONS 138110, S44127

REFERENCE A55636

Authors Volinia, S.; Hiles, I.; Ormody, E.; Nizetic, D.; Antonacci, R.; Rocchi, M.; Waterfield, M.D.

#journal Genomics (1994) 24:472-477

#title Molecular cloning, cDNA sequence, and chromosomal localization of the human phosphatidylinositol 3-kinase p110 alpha (PIK3CA) gene.

#cross-references MUID:95229146

#accession 138110

#status preliminary

#molecule_type mRNA

#residues 1-1068 #label RES

#cross-references EMBL:Z29090; NID:9472990; PID:9472991

GENETICS

#gene GDB:PIK3CA

#cross-references GDB:370915; OMIM:171834

#map_position 3q26.3-q28.3

CLASSIFICATION #superfamily phosphatidylinositol 3-kinase

KEYWORDS phosphotransferase

SUMMARY #length 1068 #molecular-weight 124411 #checksum 9584

Query Match 13.4%; Score 1151; DB 2; Length 1068;

Best Local Similarity 30.7%; Pred. No. 4,736-187;

Matches 240; Conservative 211; Mismatches 267; Indels 64; Gaps 41;

Db 326 SLWVYNRLRIK-ILCATVYNLRIDIDKIYRT--GIYHGEPICDNVNTQVPCSNPR 382

QY 385 SLMDLADNLRPNVNSG-FDPA-DVD-MYRIEFSYVGLTLTASK-STTKYNAOPAK 440

Db 383 WN-EWLANDIYIPDPRARCLSTICSVKGRKGAKEHCPLANGNINLFOTDTLVSGKM 441

QY 441 WNKEMTYTDLTKMDMPSA-V-LSIRLYGKVKLSEEEFGVGNMSTLTDWDELROGQF 498

Db 442 ALNLMPVHGLEDLNPFGVTSNPNKETPCLELEPFDFSSVVKFPDKSVIEEHNANSVS 501

QY 499 LFHLMA-PEPTANR-SRIGENGARIGTAA-VTIEISSYGRVAMP--S--QGYTYLVK 551

Db 502 REAGFSYSHAGLSNRLANDLRENDKEQLAISTRDLPSITEQKD-FLMSHRHCYT 560

QY 552 HRSTWETLINMGDDY--ESCIRDPGYKRLQMLVKHSGIYLEDDEORHVMWRRYIQK 609

Db 561 -IPELPLLL-LSVKWNRSDEVAOMCYLKYMPPIKPPQANELLDCNTPDMVNGFAVRC 618

QY 610 QEPDLILVSELAFTWDRENSELYVMLEKKKPPSVAALTLGLKRCCTDRYIRKFAVEK 669

Db 619 LEKYTDDKLSQYLQVLYQVLEKQYLDNLLVRELFLLKATLNRGHPFHLKSE---M 675

QY 670 LNEQLSPYTFHFLPLQALKYEPRAOSEVMMLTRALCDYRIGHRLFMILRAELARL 729

Db 676 HN---KTVS-ORFGLLESYGRACGMYLKHLNROYEANEKILNTDILIKOKRDETOVKQ 731

QY 720 RDCDLKSESEYRISILMEAYILRGNEEHKIIIRQVDVDELTRISTLVKGMKDYA--T- 786

Db 732 MKFLVEQARRRDFMDALOGLLSPINPAHQGNLKEKRIMSSAKRPLMLWNEPDIMSE 791

QY 787 MK-LNDELIR-S-ISHKMNMDSPIDPYKKGEMIIDKAIYLSGAKRPLMLMKKNKPSD 843

Db 792 LLFQNNELFRNGDILRODMTLTIIRIMENIMONOGDLMPLPYGGLSISDGLIEVY 851

QY 844 LHLPCAMIFKNGDILRODMVLYOLEVMDNIMKRAANDCCLNPAVALPMGEMIGIIEVY 903

Db 852 RNSHTIMQIOCKG-LKGALO-FNSHTLHOWL-K---D-KNRG-EIY-DA-A--ID- 895

QY 904 PNCKTIFELIYGTGFMNTAVRSIDPSFNKKIRKOCGIEDEKKSCKDSTNPIEKKIDN 963

Db 896 ---L---F-T--R---SCAGYCATFTIGIDRHSNINMVDQDLPHIDGHLDRKKK 943

QY 964 TQAMKKTIESYDRFLYSCVGSVATYIMGIDRHSNIMLTEDKRYHIDGHILGKTK 1023

Db 944 KFGYREKREPVLYMODFLIVSKGQECTKTRERFEOEMKYKYLALROHANTFINFS 1003

QY 1024 KLGIORDROPILTEHEFTVIRSGKSVDSGNSHELOKFTLCEVAYEVMMNNRDLFVSLFT 1083

Db 1004 KMLGSGMPELOSFDIAYIRKTL-ALDKTEQALEYFKKONMDAHGCGWTKMDIETFI 1062

QY 1084 LMLGMELEPSTKADLDHLKTLFCNGESKEARKEAFGIYEEAFNGSWSKTITWMLFRAV 1143

Db 1063 KQ 1064

QY 1144 KH 1145

```
RESULT 3
ENTRY 3
TITLE A43322 #type complete
ORGANISM phosphatidylinositol 3-kinase 110K chain - bovine
DATE #formal_name Bos primigenius taurus #common_name cattle
04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
29-Jan-1999

ACCESSIONS
REFERENCE A43322
#authors Hiles, I.D.; Otsu, M.; Vollmar, S.; Fry, M.J.; Gout, I.;
Dhand, R.; Panayotou, G.; Ruiz-Larrea, F.; Thompson, A.;
Totty, N.F.; Hsuan, J.J.; Courtneidge, S.A.; Parker, P.J.;
Waterfield, M.D.
#journal Cell (1992) 70:419-429
#title Phosphatidylinositol 3-kinase: structure and expression of
the 110 kd catalytic subunit.
#cross-references NID:92354059
#accession A43322
#status preliminary; not compared with conceptual translation
#molecule_type nucleic acid; protein
#residues 1-1068 #label HIL
#cross-references GB:M93252; NID:g163519; PID:g163520
#experimental_source brain
#note sequence extracted from NCBI backbone (NCBI:P110292)
CLASSIFICATION #superfamily phosphatidylinositol 3-kinase
SUMMARY #length 1068 #molecular_weight 124327 #checksum 8628

Query Match 13.4%; Score 1151; DB 2; Length 1068;
Best Local Similarity 30.7%; Pred. No. 4.73e-187;
Matches 240; Conservative 212; Mismatches 266; Indels 64; Gaps 41;

Db 326 SLWVINSALRIK-ILCATYVNVNIRIDIKIVRT--GIYHGEPDLDNVTQHPVCPNPR 382
OY 385 SLWDLDMANIRVNVISGF-DEPA-DVD-MYVRIEFSVYVGLTLASK-STTVNNAQAK 440
Db 383 WN-EMLNIDYIPDLPRARLCSICSVKGRKAKKEHCPLANGNINLFYDTLVSGKM 441
OY 441 WNKEMTFTDLYKMDMPSA-V-LSIRVLKVKLKSEEFVGVNWSLTDMDRLRQGP 498
Db 442 ALNLMPVPHGLDLPNIGVTSNPNKPTPCLLEFDMFESVYKFPDMSTIEHANKSVS 501
OY 499 LFLPLM-PEPTANR-SRIGNSGARIGTMA-VTEISSTGGVRMP--S--QGGYTYLVK 551
Db 502 REAGFSYSHAGLSNRLARDELRENDKEQRAICTRDLSEITEQEKD-FLMSHRHYCVT 560
OY 552 HRETWTETLINMGDDV--ECCIRDPGVKKIQLMKKHESIYVEEDQRVYMMKRIQK 609
Db 561 -IPEILPKLL-LSKWNNSRDEVAQNTCLVKNPPIKPEQAMELLDCNYDPNVRGEAVRC 618
OY 610 QEPDLILVSELAFVWTDRENFSELYMLEKMPPSVAALTLGKRCSTRVIRKFAVEK 669
Db 619 LEKYLDDKLSQVLIQVLYLKYEQYLDNLVFLKALTNORIGHFFVHLKSE--M 675
OY 670 LNEQLSPVTFHFLPLQLQKTEPRASQSEVGMMLTLTRACDRIGRHLEWMLRAELARL 729
Db 676 HN--KTVS--QREGLLESYCRACGMYLKHLNROVEAMEKLINLTDLKOEKKDEQKQ 731
OY 730 RQDDKSESEYRISLMEATLRGNEEHKIKITIQVMDVLDTRISILYKMPDVA--T- 786
Db 732 MKFLVQMRPDMALQGLFSLPNPAHQNLRLBECRISSAKRPLMLNENPDIMSE 791
OY 787 MK-LRDELRL-S-ISHKKNENDSPLDPYKIGEMIIDKAIYVLSAKRPLMLHMKRNP 843
Db 792 LLEQNNEILFKNGDDLRODMLTQIIRIMENINONGDLRLMPLPGCLSLGDCVGLIEV 851
OY 844 LHPFCAMLTKNGDDLRODMLTQVLEVMNIMKANIDCLNPPYAVLPGGEIGIIEVV 903
Db 852 RNSHTIQQICGKG-LKGAQ-FNSHTLQWL-K-----D-KNKG--EIT-DA-A--ID- 895
OY 904 PNCKTIFELIOVGTFMNTAVRSIDPSFMNKKIRKQGIIEBKSKSDSTKNPEIKKIDN 963
Db 896 ---L---F-T--R---SCAGYCVATPLIGIGDRHNSNIMVWDQGLFHLIDFGHLDK 943
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QY 964 TQAMKRYFESVDFELYSQVYSVATYIMGIRKDRSDNMLTDEGKYVHIDFGHILHGRT 1023
Db 944 KEGYKREVPFVLTQDFELVVISGAQECTRTREEFQEMCKAYALAIQHANLFINLRS 1003
OY 1024 KGIQDRQPFILTEFKYVINSKSVDSNHELQFKTLCEAYEVMMNRDLFVSLFT 1083
Db 1004 MMLSGMPELOSFDDIAYIRKTL-ALDKTEQALLEYFMQMDAHHGWTTKMDWFTRT 1062
OY 1084 LMGMLPELSTRADLDHKLKTLFCNGESKEARKKFAIYEAFNGSSTKTNLWLFHAV 1143
Db 1063 KQ 1064
OY 1144 KH 1145

RESULT 4
ENTRY 4
TITLE A54600 #type complete
ORGANISM phosphatidylinositol 3-kinase 110K chain isoform beta - human
DATE #formal_name Homo sapiens #common_name man
25-Oct-1994 #sequence_revision 18-Nov-1994 #text_change
29-May-1998

ACCESSIONS
REFERENCE A54600
#authors Hu, P.; Mondino, A.; Skolnik, E.Y.; Schlessinger, J.
#journal Mol. Cell. Biol. (1993) 13:7677-7688
#title Cloning of a novel, ubiquitously expressed human
phosphatidylinositol 3-kinase and identification of its
binding site on p85.
#cross-references NID:94067128
#accession A54600
#status preliminary
#molecule_type mRNA
#residues 1-1070 #label HUI
#cross-references GB:S67334; NID:g455759; PID:g455760
#note sequence extracted from NCBI backbone (NCBI:P140879,
NCBI:P140880)
GENETICS
#gene GDB:PIK3CB; PIK3C1
#cross-references GDB:136233
CLASSIFICATION #superfamily phosphatidylinositol 3-kinase
SUMMARY #length 1070 #molecular_weight 122761 #checksum 7198

Query Match 11.7%; Score 1011; DB 2; Length 1070;
Best Local Similarity 34.1%; Pred. No. 6.47e-160;
Matches 233; Conservative 170; Mismatches 217; Indels 63; Gaps 43;

Db 436 YPYAVWNTVDFEKGQLRTGDIILHSWSSFPELEMLNPMGT-VQNP-YT-ENAT-AL 491
OY 477 FEYGVNMSLTDWRDELROGOEFLHMAPEPTANRSRIGENGARIGTNAVTEISSYG 536
Db 492 HYKFPENKQPIYPYFPDILIT-EKAAEIASSDSAN-VSSRGCKKPLPYLKEILDRPPLQ 549
OY 537 RVAMP-SQGO-TYLYVKNHSTWETELINGDDYESCIRDPGVKK-LQML--VKKHSGIV 591
Db 550 LCENEMDLIMTLRODRELEFPOSPLKLL-LSIKWNKLEDAVQALQIOLIMPLRP-REAL 607
OY 592 LEEDEQRHVMKRYIQKQEPDLILVSELAFVWTDRENFSELYVLEWR-KPSSAAL 650
Db 608 ELIDFNYPQVYREYAVGLR-QMSDELSQVLIQVLYLKYEPFLDCAISRLELRALG 666
OY 651 TLGKRCSTRVIRKFAVEKLEBQSPVTFHFLPLQLQKTEPRASQSEVGMMLTLTRALC 710
Db 667 NRIQGFLEWHLRSEY-HIPL--V-SVQGV-V-IL-EATCRGSVGMKYLKSOVEYLANL 719
OY 711 DYRIGRLFWMLRAETARLDCDLKSEYRISLMEAYLRGNEEHKIKITRQVADVDEL 770
Db 720 KTLNSILKINAVLNLRKAKKEAMHTCLKQSAVREALSDQSPINPVIISLEYVECKYM 779
OY 771 TRISTILVK-GMPR-DVATYK--LRDELRSISHK--MENNDSPLDPYKIGEMIIDKAIYV 824
Db 780 DSKMKPLMLVYNKVF-GE-D-SV-GVIFKNGDDLRODMLTQIOMLRMLDLKREAGLDLR 835
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QY 825 GSAKPLMLHMKNNKPSDLHLPCAMIFKNGDDLRODMLVQLEVMNDIMKANIDCC 884
DB 836 MLPGCLATGDRGSLIEVSTSETTADIDOLNSSNVAFAFNKDALIN-WL-KEY---NS 890
QY 885 LNPVAVLPGEMIGIIEVVPNCKTIFELIOVGFMNTANRSDPSMNMWIKKOCIEDE 944
DB 891 ---G---D-LDRAIE--E-----F-T---L-SCAGYCAASYVLGIGDRHSDINWK 928
QY 945 KKRSKRSSTKPNIEKKIDNTQAMKRYFESVDRLFCVSVATYIMGIDKDRHSDINMLT 1004
DB 929 KTGOLFHDGHIILGNFKSGFKIRREVPFLLTYDPIHYIOGKT--GNTKRGFRQCC 986
QY 1005 EDGKVVHIDFGHILGKTKGIDRROPFLLTEHMTYINSKGSVDGSHELQKFTLC 1064
DB 987 EDAYLLRRHGHILFTFLFALMLTAGLPFLTYSKDIQYLLKDSL-ALGSESEALKOFKOF 1045
QY 1065 VEAIVEMNNRDLFVSLFTLMGMLPELSTKADLDHLKTLFCNGESKEARKEPFAIGY 1124
DB 1046 DEALRESWTTKVNNMAHYRKDY 1068
QY 1125 EEAFGNSMSTKTNMLFHAV-KHY 1146

RESULT 5
ENTRY A57134 #type complete
TITLE phosphoinositide-3 kinase - human
ALTERNATE_NAMES p110-gamma protein
ORGANISM #formal_name Homo sapiens #common_name man
DATE 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 17-Mar-1999

ACCESSIONS A57134
REFERENCE A57134
AUTHORS Stoyanov, B.; Volinia, S.; Hancock, T.; Rubio, I.;
Loubtchenkov, M.; Malek, D.; Stoyanova, S.; Vanhaesebroeck,
B.; Dhand, R.; Nuerberg, B.; Gierschik, P.; Seedorf, K.;
Hsuan, J.J.; Waterfield, M.D.; Wetzker, R.
#journal Science (1995) 269:690-693
#title Cloning and characterization of a G protein-activated human
#cross_references MUID:95350661
#accession A57134
#status preliminary
#molecule_type mRNA
#residues 1-1050 #label STO
#cross_references GB:X83368
GENETICS
#gene GDB:PIK3CG
#map_position 3q26.3-q26.3
#classification #superfamily phosphatidylinositol 3-kinase
SUMMARY #length 1050 #molecular_weight 120444 #checksum 5420

Query Match 10.7%; Score 925; DB 2; Length 1050;
Best Local Similarity 33.1%; Pred. No. 2,40e-143;
Matches 216; Conservative 171; Mismatches 204; Indels 62; Gaps 31;

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QY 717 RLFWLRAEIALRDCDDKSEERISILMEAYLNG--NEEHIKITTRQVDWDELTRIST 775
DB 714 DIKSLAKRYDVSSOVISOLKOKLENLONSQLPSEFRVPYPGKAGALATECKVMASK 773
QY 776 LYKGNP--K-DVAT--M-KLDELRSISH-KK-EMMSPLDPYKLGSMITDKAIVLQSA 827
DB 774 KKPWLFEKCAPDPA-TSNETIGILFKHGDDLRODMLLIQILRIMESIWETESIDLCLP 832
QY 828 KRPMLHMKNNKPSDLHLPCAMIFKNGDDLRODMLVQLEVMNDIMKANIDCCNP 887
DB 833 YGCISTGKIGHIEIVKATITAKIQSTV--GNIG--AFKREVLNHL-K-----EK-- 880
QY 888 YAVLPMGEMIGIIEVVPNCKTIFELIOVGFMNTANRSDPSMNMWIKKOCIEDEKK 947
DB 881 ---S---PTEKEF---QA-----AVRFYSCAGYVATFVLGIGDRHSDINMITEG 924
QY 948 SKKSTKPNIEKKIDNTQAMKRYFESVDRLFCVSVATYIMGIDKDRHSDINMLTIDG 1007
DB 925 MLFHIDFGHILGNFKSGFKIRREVPFLLTYDPIHYIOGKT--GNTKRGFRQCC 986
QY 1008 KYVHIDFGHILGKTKGIDRROPFLLTEHMTYINSKGSVDGSHELQKFTLCVYA 1067
DB 983 YLALHHTNLLITLFSMMLTGMPTLSEKEDIEYRLAL-TVGNKEDEAKRYF 1034
QY 1068 YEVMNNRDLFVSLFTLMGMLPELSTKADLDHLKTLFCNGESKEARKEPFAIGY 1124

RESULT 6
ENTRY JC5500 #type complete
TITLE phosphoinositide 3-kinase (EC 2.7.-.-) - human
ALTERNATE_NAMES #formal_name Homo sapiens #common_name man
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 29-May-1998

ACCESSIONS JC5500
REFERENCE JC5500
AUTHORS Brown, R.A.; Ho, L.K.F.; Weber-Hall, S.J.; Shipley, J.M.;
Fry, M.J.
#journal Biochem. Biophys. Res. Commun. (1997) 233:537-544
#title Identification and cDNA cloning of a novel mammalian C2
#cross_references MUID:95350661
#accession JC5500
#status preliminary
#molecule_type mRNA
#residues 1-1634 #label BRO
#cross_references GB:Y11312; NID:q2076603; PID:e311430; PID:g2076604
#experimental_source breast cell
#COMMENT This enzyme is involved in receptor signal transduction, in a
signaling complex which mediates intracellular protein
trafficking, and in the regulation of cell proliferation and cell
survival.
GENETICS
#map_position 1q32
#classification #superfamily Hsc2 phosphatidylinositol 3-kinase; protein
#keywords kinase C C2 region homology; PX domain homology
#feature
156-162,169-174 #domain SH3 #status predicted #label SH3\
809-968 #domain phosphoinositide,3-kinase #status predicted
#label PIKX
1037-1320 #domain catalytic #status predicted #label CATY
1495-1634 #domain C2 #status predicted #label C2D\
SUMMARY #length 1634 #molecular_weight 184856 #checksum 1177

Query Match 7.2%; Score 621; DB 2; Length 1634;
Best Local Similarity 30.7%; Pred. No. 1.09e-85;
Matches 180; Conservative 140; Mismatches 208; Indels 58; Gaps 35;

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OY 626 TDRENFSELYWLEKWKPPSVAALTLGLKCTDVIKFAVEKNEQLSPVTFHLFTLP 685
OY 922 LVQALKYCYLDSPLVRLKRAVSDLRTHYEFMLK-D-G-LKDSOF-SIRYO-Y-TL 975
OY 666 LIQALKYPRASOEGMMLLRALCDYRIGHRLFWLLRAELARLDCCLSKEYSRISLL 745
OY 976 -AALLCCGKGLREFFNRQCLVNALAKLAQVREAPASAROGILRTGLEEYKOPFALNG 1034
OY 746 MEAYLRNGEHEHKI-ITRQVDMVDDELTRISTLVKGMKPDVATMKRLDELRSISHKME-NM 803
OY 1035 SCRPLPSLS-LVKGIVRDCSYFNSNAVPLKLSFQNDPLGE-NIR--VIFKCGDLR 1089
OY 804 DS--PLDVPYRLGEMIDKAIY-LGSARPLMLHMKNNPKSDLLPFCAMIFKNGDILR 860
OY 1090 QDMTLQMRIRMSKIWVOEGDMRVIFRCFSTGRGAVEMIPNAETLRKIOVHG-VT 1148
OY 861 QDMVLVQVLEWMDNIMKAAANIDCCLPAYALPMGEMIGIIEVVPCKTIFELQVGTGFMN 920
OY 1149 GSFK--DRP-LADWL--Q-----KH--NPGE--DEYE--K--AVENFIYS 1180
OY 921 TAVRSIDSPFMKWKIRKCGIEDEKSKSKDSTKNPIEKKIDNTQAMKKYFESVDRLYS 980
OY 1181 CAGCCVATYVIGICDRHNDIMTKTGGMFHDGFRFLGHQO-MGNTKRDPAFVFTSD 1239
OY 981 CVGSVATYVINGIKDRHSDNMLTEDGKYVHIDFGHILGHGKTKLG-TORDROPILTEH 1039
OY 1240 -MAYVING-GDKPSR-FHDFVLDCCQAVNLIRKTHLFNLGLMLSGIPSLDLDL 1296
OY 1040 FMTVIRSRKSDVNSHELOKFKTLCVEAVEYWMNNRDLFVSLFTMLGMEPELSTKADL 1099
OY 1297 RYVYDALRPQ-DTEANATYFTRLISSL-GSVATKLNFEIHNLAQ 1340
OY 1100 DMLKTLFCNGSKREARKFAGIYEAFNGSWSTKTMFLFAVXH 1145

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RESULT 7

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ENTRY JC5985 #type complete
TITLE phosphoinositide 3-kinase C2gamma - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 06-May-1998 #sequence_revision 29-May-1998 #text_change 17-Mar-1999

```

ACCESSIONS

REFERENCE JC5985

authors Misawa, H.; Ohtsubo, M.; Copeland, N.G.; Gilbert, D.J.;

journal Jekins, N.A.; Yoshimura, A.

title Blochem. Biophys. Res. Commun. (1998) 244:531-539

cross-references MIM:291891

accession JC5985

residues 1-1506 #label MIS

cross-references DDBJ:AB08791

comment This protein exclusively expressed in the liver, and a N-terminal

truncated form is found in lung and a certain hema topoletic cell

line.

GENETICS #map_position 6

CLASSIFICATION #superfamily Hsc2 phosphatidylinositol 3-kinase; protein

FEATURE #domain catalytic #status predicted #label CAT

SUMMARY #length 1506 #molecular_weight 171659 #checksum 9731

Query Match 7.0%; Score 599; DB 2; Length 1506;

Best Local Similarity 30.2%; Pred. No. 1.35e-81;

Matches 173; Conservative 134; Mismatches 214; Indels 51; Gaps 32;

DB 716 KHAKLSOKK-SPLLSSEKRYLWFYRLXCNENSSLPVIGASP-GWDE-ETVSEKHA 772

OY 577 KKLQWLKHHESGIVLEDEORHVMRRYIQKQEPDLIVLSLAFWTDENSELYV 636

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DB 773 ILRRWTSHPMEALGLTSRPPDDIREVAVOQDITLTD-EL-LDCLPOLQAVKEWN 830
OY 637 MLEKWKPPSVAALTLGLKCTDVIKFAVEKNEQLSPVTFHLFTLP-LIQALKYPR 695
DB 831 LESPLVELPRPLOSIRVANCILYWLAR-D-AQGEAY-FKSW-YQELLALQFAGELN 886
OY 696 AQSEVGMMLLRALCDYRIGHRLFWLLRAELARLDCCLSKEYSRISLLMEAYLRNG-E 754
DB 887 EELSNEOKVLLADIDIGEKVKSASDPOKQVLLKEI-GSLSEFPKDIKCHLPALCI 945
OY 755 EHKITTRQVDMVDDELTRISTLVKGMKPDVATMKRLDELRSISHKME-NM 813
DB 946 KGIDRACSYTSNAPSLKTFINANPKG-NI--SVIFRAGDRLRQDMLALQIYMD 1001
OY 814 GEMIIDKAIYVGSARPLMLHMKNNPKSDLLPFCAMIFKNGDILRQDMLVQVLEWMD 873
DB 1002 NAWLOEGDMQITTYGCLSTRAGQFIEMVDPAVTLAKIHLHSLIG-PLK-ENT-1KK 1057
OY 874 NIMKAAANIDCCLPAYALPMGEMIGIIEVVPCKTIFELQVGTGFMNTAVRSIDSPFMK 933
DB 1058 WFS-Q--HNHLK---E--D-YEK-----ALRN-F-----F-YSCAGCQVTFILGV 1092
OY 934 WIRKQCGIEDKSKSKDSTKNPIEKKIDNTQAMKKYFESVDRLYSVATYVIGI 993
DB 1093 CDRHNDIMTKTGGMFHDGFRFLGHQO-MGNTKRDPAFVFTSE-MEYFITE-GGK-N 1149
OY 994 KDRHSDNMLTEDGKYVHIDFGHILGHGKTKLG-TORDROPILTEHFMVIRSRKSDVGN 1053
DB 1150 IQHODEVELCCRAVNYRKISOLISLEMLHAGLDELGIDLYKVNHLNRPQ-DTD 1208
OY 1054 SHELOKFKTLCVEAVEYWMNNRDLFVSLFTMLGMEPELSTKADLHKLKTLFCNGESK 1113
DB 1209 LEATSHFTKTKKESE-CFYPKLNLTHTLQ 1239
OY 1114 EARKFFAGIYEAFNGSWSTKTMFLFAVXH 1145

```

RESULT 8

```

ENTRY PC4002 #type fragment
TITLE phosphatidylinositol 3 kinase (EC 3.1.3.-) - fission yeast
ORGANISM #formal_name Schizosaccharomyces pombe
DATE 29-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 17-Mar-1999

```

ACCESSIONS

REFERENCE PC4002

authors Kimura, K.; Miyake, S.; Makuch, M.; Morita, R.; Usui, T.;

journal Yoshida, M.; Horiouchi, S.; Fukui, Y.

title Biosci. Biotechnol. Biochem. (1995) 59:678-682

cross-references MIM:291891

accession PC4002

residues 1-664 #label KIM

comment This protein exclusively expressed in the liver, and a N-terminal

truncated form is found in lung and a certain hema topoletic cell

line.

GENETICS #gene

KEYWORDS #length 664 #checksum 6458

SUMMARY #length 664 #checksum 6458

Query Match 5.3%; Score 456; DB 2; Length 664;

Best Local Similarity 29.1%; Pred. No. 2.13e-55;

Matches 166; Conservative 134; Mismatches 201; Indels 70; Gaps 44;

DB 145 LSLERKDLIMKREFYLRNKKAMTKFLKSV--VWDSSEVQALSLDSWTEIDDALE 202

OY 592 LEEDQORHVMRRYIQKQEPDLIVLSLAFWTDRENFSELYWLEKWKPPSVAALTL 651

DB 203 LLSFVHPKRAYAVSL-ETASNEELLVLDLQVQALRKDNRTSSDERQSPALFL 261

OY 652 LLGRKCTDVIKRAVERKNEQLSPVTFHLFTLP-LIQALKYPR 704

```

Dh 262 VNRAISSPSINDNDXYLVLAWEIE--D-EVSKLSESSVMEFLQKELSKSVEGLIRETUS 317
Qy 705 LTRALCDYRIGHRLFWMLLRREIARLNRCDCLSKSEYKRISLSLMAYL-RGNHEH-1K-IIT 761
Db 318 AQANFVEKRLRISKSVSOFKTRIKLKEYLKVLLEDHKHLLDFFALPLPLDPSVNIIGI 377
Qy 762 ROYVMDELTRISLV--KGMp-KDVA7MK-LRDELRSISHKEMNDSPLDPPVYLCEM 816
Db 378 IPDACYFKSRMOPLRLFLFCODG-SK-----Y-PIIFKNDDLRQDOLYOLITLMDKLL 431
Qy 817 IIDAIYUGSKRRPLMLHKKNKPNKSOHLRPFQAMIFKNSDDLROMLVQVLEVDNDIM 876
Db 432 KKEKLDLHLKEPYRIATGPTHGAVQVPS-KTIA1I-L-AEY-HGSV-L-AYL----R 479
Qy 877 KANIDCCLNPYAVLPPMGEMIGITIEVPYCNKTFEIQVGCGFWNTAVRSIDPSFNKWR 936
Db 480 -E-NNPDD--GL-NSA-N-YG--IDPV-AMDY--V-R---TCAGYCYITTYLGVGR 521
Qy 937 KQCGIEDKKSKSDKSNPKLEKIDMTQAMKKYFESVDVFLISCVGYSVATYIMIKR 996
Db 522 HLDNLLITKDFHFAADFGYLLGD-PKL-F-S-PAMKLSKE-M-V-EGMG-GYNSPF 571
Qy 997 HSDNMLTEODKYVHIDFGHILGSGKRLDIOQDRQFILLTEHFMVYINSKSGVDSNHE 1056
Db 572 YQOKRSYCYITFTLKRSSNLIILWESLAVDANIPDIKEDKRVYVYKVERFLQMSD 631
Qy 1057 LQKFKTLCEAVEYEWMMNRDLFWLSFLITLMGMELPETS-TKAOLDHLKTYLPONGESKE 1111
Db 632 AIKFEQOLINNSVALFPQIIDRM-NHLYQ 661
Qy 1116 AKKEFFAGIYEAFNGSWSTKTNMLFEHAVKRY 1146

```

```

RESULT      9
ENTRY
TITLE      A59003      #type complete
ORGANISM    phosphatidylinositol 3-kinase - slime mold (Dictyostelium
DATE        discoidium)
ACCESSIONS  #format_name Dictyostelium discoidium
REFERENCE   15-Aug-1997 #sequence_revision 15-Aug-1997 #text_change
#authors    29-Jan-1999
#journal     A59003
#title       A59003
            Zhou, K.; Takegawa, K.; Emr, S.D.; Fittell, R.A.
            Mol. Cell. Biol. (1995) 15:5645-5656
            A phosphatidylinositol (PI) kinase gene family in
            Dictyostelium discoidium: biological roles of putative
            mammalian p110 and yeast Vps34p PI 3-kinase homologs during
            growth and development.
            #cross-references MIMD:96009592
            #accession    A59003
            #status       Preliminary
            #molecule_type mRNA
            #residues     1-816 #label ZHO
            #cross-references GB:U23480; NID:g733529; PID:g733530
            #superfamily slime mold phosphatidylinositol 3-kinase
            SUMMARY      #length 816 #molecular-weight 94646 #checksum 731

Query Match      4.5%: Score 384; DB 2; Length 816;
Best Local Similarity 29.1%: Match No.1,40e-42;
Matches 151; Conservative 125; Mismatches 171; Indels 72; Gaps 48;

Db 309 IMRRRYLTNNKALTFELRCVE--VSESHQKNKALSIM-PMWDPIDIDSELLSFAFT 365
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 600 VMMRRRYIQKQEPDLLIVLESLAFWMTD-RENSSELYVLEKMKPPSVAALITLIGKCT 658
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Db 366 HKNTIMARRAVELKRA-DDEELLYILLOVQATYEEQFDGPNPSDPLISFLERSKN 424
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 659 DR--V-IRKFAVEKLNQLSPVTFHFLIPLIDALKYEP-RAQ-SEVGKM--LTLRALCD 711
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Db 425 FILSHFWYLTVDVSYSKSSIFCSHYKTYOELFYRDLH-TDA-QRVNQN-KFISRLSL 481
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 712 YRIGRLFWLRLRAI-IARLND-CD-LKS-BE-Y-RIISLMEYVLENGNEHKRIITTRVD 765
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

[illegible]

RESULT	10
ENTRY	A36369
TITLE	vacuolar protein-sorting protein VPS34 - yeast (<i>Saccharomyces cerevisiae</i>)
ALTERNATE_NAMES	protein L9672.10; protein YNR240w
ORGANISM	#formal_name <i>Saccharomyces cerevisiae</i>
DATE	28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 06-Feb-1998
ACCESSIONS	A36369; S59386
REFERENCE	A36369
#authors	Herman, P.K.; Emr, S.D.
#journal	Mol. Cell. Biol. (1990) 10:6742-6754
#title	Characterization of VPS34, a gene required for vacuolar protein sorting and vacuole segregation in <i>Saccharomyces cerevisiae</i> .

[illegible]

QY 1034 FILEHEMTVIRSGKSVDSGSHLOKFKTLCEAVEYEMNNRDLFVSLFTLMGLMELPEL 1093

DB 820 RIDPNGAILVEREPFINNSEEDATVHFONLINDSVALLPIVIDHL-HNLAOY 872

QY 1094 STRADIDLK-KTLFCNGESKEARKEFFAGIYEAFNGSWSTKTNLHFVAKHY 1146

RESULT 11

ENTRY PC4348 #type fragment

TITLE phosphoinositide 3-kinase (EC 2.7.1.119) T119 - human

ORGANISM (fragment)

DATE 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 26-Feb-1998

ACCESSIONS PC4348

REFERENCE PC4345

#authors HO, L.K.F.; Liu, D.; Rozyczka, M.; Brown, R.A.; Fry, M.J.

#journal Biochem. Biophys. Res. Commun. (1997) 235:130-137

#title Identification of four novel human phosphoinositide 3-kinases defines a multi-isoform subfamily.

#accession PC4348

#status nucleic acid sequence not shown

#molecule_type mRNA

#residues 1-133 #label HOA

COMMENT This enzyme plays a role in diverse cellular processes including cell migration, cell proliferation, oncogenic transformation, cell survival and intracellular trafficking of proteins.

CLASSIFICATION #superfamily phosphatidylinositol 3-kinase

KEYWORDS phosphotransferase

SUMMARY #length 133 #checksum 4564

Query Match 2.9%; Score 253; DB 2; Length 133;

Best Local Similarity 42.0%; Pred. No. 2.23e-20;

Matches 34; Conservative 19; Mismatches 27; Indels 1; Gaps 1;

DB 1 GDRLQDMTLQMEIMLVLMKQEGDLRMTPYGLPTGDRGLTEVYLRSDTINOLN 60

QY 856 GDRLQDMTLQMEIMLVLMKQEGDLRMTPYGLPTGDRGLTEVYLRSDTINOLN 60

DB 61 KSNMATAFNKDALIN-WLK 80

QY 916 TGFMTAVRSIDPSFMNKMIR 936

RESULT 12

ENTRY S57219 #type complete

TITLE phosphatidylinositol 3-kinase - human

ORGANISM #formal_name Homo sapiens #common_name man

DATE 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 03-Nov-1995

ACCESSIONS S57219

REFERENCE S57219

#authors Vollmar, S.; Dhand, R.; Vanhaesebroeck, B.; MacDougall, L.K.; Stein, R.; Zvelebil, M.J.; Domin, J.; Panaretou, C.; Waterfield, M.D.

#journal EMBO J. (1995) 14:3339-3348

#title A human phosphatidylinositol 3-kinase complex related to the yeast Yps34p-Yps15p protein sorting system.

#cross-references MIMD:95354652

#accession S57219

#status preliminary

#molecule_type mRNA

#residues 1-887 #label VOL

SUMMARY #length 887 #molecular-weight 100918 #checksum 6781

Query Match 2.9%; Score 253; DB 2; Length 887;

Best Local Similarity 34.4%; Pred. No. 2.23e-20;

Matches 54; Conservative 32; Mismatches 60; Indels 11; Gaps 8;

DB 720 EVMNTYKSCGCVITYIIGVGRHNDLVLTGKLFHIDEGYILIGRD-PK-PLD--- 774

QY 972 ESDVRLTSCGVSVATYIMGKDRHSDNMLTEDGYVHIDFGHIGKTKIGIORDR 1031

DB 775 PPMKLNKE-M-V--EGMG-GTQSEGYQEFRRQCYTAFLRLRYNLINLSLWDPNIP 829

QY 1032 QPFIETHEMTVIRSGKSVDSGSHLOKFKTLCEAVEYEMNNRDLFVSLFTLMGLMELP 1091

DB 830 DIALPPDKTVKQVQDKFKLSDSEAVHYMQSLIDES 866

QY 1092 ELSTRADIDLK-KTLFCNGESKEARKEFFAGIYEAFNGSW 1127

RESULT 13

ENTRY A55404 #type complete

TITLE 1-phosphatidylinositol 4-kinase (EC 2.7.1.67) alpha - human

ORGANISM #formal_name Homo sapiens #common_name man

DATE 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 04-Sep-1998

ACCESSIONS A55404

REFERENCE A55404

#authors Wong, K.; Cantley, L.C.

#journal J. Biol. Chem. (1994) 269:28878-28884

#title Cloning and characterization of a human phosphatidylinositol 4-kinase.

#cross-references MIMD:95050701

#accession A55404

#status preliminary

#molecule_type mRNA

#residues 1-854 #label MON

GENETICS #cross-references GB:136151; MID:9598192; PID:9598193

KEYWORDS GDB:PIK4

SUMMARY #cross-references GDB:435501

phosphotransferase

SUMMARY #length 854 #molecular-weight 96983 #checksum 9473

Query Match 2.6%; Score 227; DB 2; Length 854;

Best Local Similarity 29.3%; Pred. No. 3.02e-16;

Matches 46; Conservative 41; Mismatches 62; Indels 8; Gaps 7;

DB 691 FIRSMAYSLLEFLQIKDRHNGNIMDKRGHIIHIDFGFESSPGG-NLGWEPD-IRL 748

QY 977 FLYSCGVSVATYIMGKDRHSDNMLTEDGYVHIDFGHIGKTKIGIORDRPFI 1036

DB 749 TDE-MVINGGK-MEATP--FKWFMKCVRGYLAVRPYDAVSLVLTMDLGLPFRQ 804

QY 1037 TEHEMTVIRSGKSVDSGSHLOKFKTLCEAVEYEMNNRDLFVSLFTLMGLMELPELSTRK 1096

DB 805 T-IKLRH-FSPNMTREANFIMKVIOCSFLSNS 839

QY 1097 ADDIDLKTLFCNGESKEARKEFFAGIYEAFNGSW 1133

RESULT 14

ENTRY S65741 #type fragment

TITLE 1-phosphatidylinositol 4-kinase (EC 2.7.1.67) type 3 - bovine

ORGANISM #formal_name Bos primigenius taurus #common_name cattle

DATE 06-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 07-Feb-1997

ACCESSIONS S65741; S72615

REFERENCE S65741

#authors Gehrmann, T.; Veréb, G.; Schmidt, M.; Klix, D.; Meyer, H.E.; Varasany, M.; Hellmeyer Jr., L.M.G.

#journal Biochim. Biophys. Acta (1996) 1311:53-63

#title Identification of a 200 kDa polypeptide as type 3 phosphatidylinositol 4-kinase from bovine brain by partial protein and cDNA sequencing.

#accession S65741

#status not compared with conceptual translation

#molecule_type mRNA

#residues 1-1466 #label GEH

SUMMARY #length 1466 #molecular-weight 146600 #checksum 10984104

Query Match 2.9%; Score 253; DB 2; Length 1466;

Best Local Similarity 34.4%; Pred. No. 2.23e-20;

Matches 54; Conservative 32; Mismatches 60; Indels 11; Gaps 8;

DB 720 EVMNTYKSCGCVITYIIGVGRHNDLVLTGKLFHIDEGYILIGRD-PK-PLD--- 774

QY 972 ESDVRLTSCGVSVATYIMGKDRHSDNMLTEDGYVHIDFGHIGKTKIGIORDR 1031

 WISE (TM)

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MSPrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Fri Jul 16 17:06:16 1999; MasPar time 33.21 Seconds
 Tabular output not generated. 975.343 Million cell updates/sec

Title: >US-08-908-453-1
 Description: (1-1146) from US08908453.pep
 Perfect Score: 8617
 Sequence: 1 MHVNIHLHPQLQTVMEQOMR.....AFNGSMSTKTNLHFHAVKHV 1146

Scoring table:
 PAM 150
 Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot37
 1:swissprot

Statistics: Mean 57.005; Variance 101.644; scale 0.561

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	8617	100.0	1167	1	AGEL_CAEEL	PHOSPHATIDYLINOSITOL 3	0.00e+00
2	1161	13.5	1068	1	PI1A_MOUSE	PHOSPHATIDYLINOSITOL 3	2.53e-225
3	1151	13.4	1068	1	PI1A_BOVIN	PHOSPHATIDYLINOSITOL 3	5.28e-223
4	1151	13.4	1068	1	PI1A_HUMAN	PHOSPHATIDYLINOSITOL 3	5.28e-223
5	1011	11.7	1070	1	PI1B_HUMAN	PHOSPHATIDYLINOSITOL 3	1.20e-190
6	981	11.4	1102	1	PI1C_HUMAN	PHOSPHATIDYLINOSITOL 3	9.62e-184
7	974	11.3	1043	1	PI1D_MOUSE	PHOSPHATIDYLINOSITOL 3	3.91e-179
8	961	11.2	1101	1	PI1D_HUMAN	PHOSPHATIDYLINOSITOL 3	6.42e-179
9	852	9.9	1858	1	P3K2_DICDI	PHOSPHATIDYLINOSITOL 3	3.24e-154
10	800	9.3	1570	1	P3K1_DICDI	PHOSPHATIDYLINOSITOL 3	2.14e-142
11	799	8.7	1585	1	P3K3_DICDI	PHOSPHATIDYLINOSITOL 3	7.35e-131
12	458	5.3	801	1	VP34_SCHPO	PHOSPHATIDYLINOSITOL 3	1.42e-66
13	344	4.5	816	1	P3K4_DICDI	PHOSPHATIDYLINOSITOL 3	6.58e-51
14	332	3.9	814	1	PI3K_ARATH	PHOSPHATIDYLINOSITOL 3	3.45e-40
15	318	3.7	814	1	P3K1_SOYBN	PHOSPHATIDYLINOSITOL 3	2.35e-37
16	297	3.4	812	1	P3K2_SOYBN	PHOSPHATIDYLINOSITOL 3	3.75e-33
17	291	3.4	1020	1	VP34_CANAL	PHOSPHATIDYLINOSITOL 3	5.80e-32
18	259	3.0	875	1	VP34_YEAST	PHOSPHATIDYLINOSITOL 3	1.01e-25
19	243	2.8	1093	1	PI4K_DICDI	PHOSPHATIDYLINOSITOL 4	1.12e-22
20	227	2.6	854	1	PI4K_HUMAN	PHOSPHATIDYLINOSITOL 4	1.10e-19
21	215	2.5	1066	1	PIK1_YEAST	PHOSPHATIDYLINOSITOL 4	1.74e-17
22	208	2.4	851	1	YDBC_SCHPO	HYPOTHETICAL 96.7 KD P	3.19e-16

24	209	2.4	1900	1	STT4_YEAST	PHOSPHATIDYLINOSITOL 4	2.11e-16
25	166	1.9	2368	1	ESR1_YEAST	ESR1 PROTEIN.	5.50e-09
26	167	1.9	2787	1	TELI1_YEAST	TELOMER LENGTH REGULAT	3.77e-09
27	155	1.8	2549	1	FRAP_RAT	FKBP-RAPAMYCIN ASSOCIA	3.25e-07
28	155	1.8	2549	1	FRAP_HUMAN	FKBP-RAPAMYCIN ASSOCIA	3.25e-07
29	145	1.7	2473	1	TOR2_YEAST	PHOSPHATIDYLINOSITOL 3	1.17e-05
30	142	1.6	2470	1	TOR1_YEAST	PHOSPHATIDYLINOSITOL 3	3.33e-05
31	109	1.3	302	1	LEX1_HAEIN	PHOSPHATIDYLINOSITOL 3	1.22e+00
32	109	1.3	312	1	FA33_RHOFA	HYPOTHETICAL 33.6 KD P	1.22e+00
33	110	1.3	528	1	CO2_MOUSE	COMPLEMENT COMPONENT C	9.19e-01
34	109	1.3	1260	1	YAOE_SCHPO	HYPOTHETICAL 138.8 KD	1.22e+00
35	110	1.3	2329	1	YL16_CAEEL	HYPOTHETICAL 272.0 KD	9.19e-01
36	109	1.3	2869	1	RBP1_PLAIV	RETICULOCYTE BINDING P	1.22e+00
37	106	1.2	334	1	HRC4_MITCA	HEAT-INDUCIBLE TRANSCR	2.85e+00
38	107	1.2	495	1	IDH_THETH	ISOCITRATE DEHYDROGENA	2.15e+00
39	107	1.2	600	1	DNL1_DESAM	DNA LIGASE (EC 6.5.1.1	2.15e+00
40	105	1.2	660	1	PL10_MOUSE	PUTATIVE ATP-DEPENDENT	3.75e+00
41	105	1.2	662	1	DDX3_MOUSE	DEAD BOX PROTEIN 3 (DE	3.75e+00
42	106	1.2	680	1	OPDA_SALTY	OLIGOPEPTIDASE A (EC 3	2.85e+00
43	105	1.2	697	1	AN3_XENLA	POTATIVE ATP-DEPENDENT	3.75e+00
44	107	1.2	734	1	NU5C_ORYSA	NADH-PLASTOQUINONE OXI	2.15e+00
45	105	1.2	827	1	GYRA_HELPY	DNA GYRASE SUBUNIT A (3.75e+00

ALIGNMENTS

RESULT 1
 ID AGEL_CAEEL STANDARD: PRT: 1167 AA.

AC 094125;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE PHOSPHATIDYLINOSITOL 3-KINASE AGE-1 (EC 2.7.1.137) (PI3-KINASE)
 DE (P1DINS-3-KINASE) (PI3K) (FRAGMENT).
 GN AGE-1.
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTIA; RHABDITIA; RHABDITIDA;
 OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERMINEA; CAENORHABDITIS.
 RN RN
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE: 96320556.
 RA MORRIS J.Z., TISSENBAUM H.A., RUVKUN G.;
 RT "A phosphatidylinositol-3-OH kinase family member regulating longevity and diapause in *Caenorhabditis elegans*.";
 RT NATURE 382:536-539(1996).
 RN RN
 RP REVISIONS.
 RC STRAIN-BRISTOL N2;
 RA MORRIS J.Z., TISSENBAUM H.A., RUVKUN G.;
 RL SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RL -1- FUNCTION: PHOSPHATIDYLINOSITOL 3-KINASE HOMOLOG THAT REGULATES LONGEVITY AND DIAPAUSE. COULD FUNCTION IN THE DEVELOPMENT OR NEUROENDOCRINE SIGNALING OF THE DAFER PATHWAY.
 CC -1- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-ID-MTO-INOSITOL - ADP + 1-PHOSPHATIDYL-ID-MTO-INOSITOL 3-PHOSPHATE.
 CC -1- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
 CC
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 CC
 CC EMBL, U56101; G1850329; -
 CC PROSITE: PS00915; P13_4_KINASE.1; 1.
 CC PROSITE: PS00916; P13_4_KINASE.2; 1.
 CC PFAM: PF00454; P13_P14_kinase; 2.
 CC PFAM: PF00613; P13Ks; 1.
 CC PFAM: PF00792; P13K_C2; 1.
 CC PFAM: PF00794; P13K_Lbd; 1.

TRANSEPERASE; KINASE.
 KM 1
 FT 847 847 S -> N (IN AGE1 (MG109)).
 FT 872 1148 PI3K/PI4K.
 FT 1167 135544 MW: 0A2A833F CRC32:
 SQ SEQUENCE 1167 AA: 135544 MW: 0A2A833F CRC32:
 Query Match 100.0%; Score 8617; DB 1; Length 1167;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 22 MHNVLHPOLQIMVEMOMKREPSLETENGKSLLENENGVADITMCPFGVIVVFPW 81
 QY 1 MHNVLHPOLQIMVEMOMKREPSLETENGKSLLENENGVADITMCPFGVIVVFPW 60
 Db 82 FLANVTSLEIKLSEKHOFLFIAPMKWGYSVKPODYVFRQLNFGIEVIFNDQPL 141
 QY 61 FLANVTSLEIKLSEKHOFLFIAPMKWGYSVKPODYVFRQLNFGIEVIFNDQPL 120
 Db 142 SKLEHGFPMFLVOPDGINRDKELMSDISHCLGSLDKLEESLDEELROFRASIMART 201
 QY 121 SKLEHGFPMFLVOPDGINRDKELMSDISHCLGSLDKLEESLDEELROFRASIMART 180
 Db 202 KKTCLTGLRGLETSYAFPEEQYLVCVSGCPKDESKVKAASLYOMFMRKRAEINGVE 261
 QY 181 KKTCLTGLRGLETSYAFPEEQYLVCVSGCPKDESKVKAASLYOMFMRKRAEINGVE 240
 Db 262 KMMKIQIEFNPNETPKSLHTEFLYEMRKLDVYDTDDPADEGFWLOLAGRTTEVTNPVXL 321
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 Db 322 TSYDGVRSLESEYRCGFVYRROSLVKDYCRPKPLIEPHYRAHRAKALDVLVSIDS 381
 QY 301 TSYDGVRSLESEYRCGFVYRROSLVKDYCRPKPLIEPHYRAHRAKALDVLVSIDS 360
 Db 382 TPKQKSNDSMTVDEFPRTASLKOVSILMDADANIMIRPVNISGDFPADVMTVRIEFSY 441
 QY 361 TPKQKSNDSMTVDEFPRTASLKOVSILMDADANIMIRPVNISGDFPADVMTVRIEFSY 420
 Db 442 VGTTLFLASKSTTKVNAQFAKMKMKEMTFDLVYMKMPASVLSIRLVYGVKLKSEEFVG 501
 QY 421 VGTTLFLASKSTTKVNAQFAKMKMKEMTFDLVYMKMPASVLSIRLVYGVKLKSEEFVG 480
 Db 502 WNMNLSITDRDELROGOFLHLMAPRPTANRSRIGENGARIGINAVTIEISSYGRVRM 561
 QY 481 WNMNLSITDRDELROGOFLHLMAPRPTANRSRIGENGARIGINAVTIEISSYGRVRM 540
 Db 562 PSQOGTYTVYKHSWTETLINMGDYESCIRDPGKKIQLMYKKHESIVLEEDQRHV 621
 QY 541 PSQOGTYTVYKHSWTETLINMGDYESCIRDPGKKIQLMYKKHESIVLEEDQRHV 600
 Db 622 WMMRRYIOKEPDLIVSELAFVWTDRENSELYVLEKMKRPPSYAALTLGKRCRDR 681
 QY 601 WMMRRYIOKEPDLIVSELAFVWTDRENSELYVLEKMKRPPSYAALTLGKRCRDR 660
 Db 682 VTRKFAVELKLNOLSPVTHFLPLIQLAKYEPRAQSEVGMMLTRALCDVRIGRLRW 741
 QY 661 VTRKFAVELKLNOLSPVTHFLPLIQLAKYEPRAQSEVGMMLTRALCDVRIGRLRW 720
 Db 742 LTRAEIARLRDCLDSEERYRISLMEAYLRGNEEHKITTROVDVDELTRISTLVKGM 801
 QY 721 LTRAEIARLRDCLDSEERYRISLMEAYLRGNEEHKITTROVDVDELTRISTLVKGM 780
 Db 802 PRDVATMKLRDELRSISHKMENNDSPLDVYKLGEMIIDKAIYVLSAKRPLMLHMKRNP 861
 QY 781 PRDVATMKLRDELRSISHKMENNDSPLDVYKLGEMIIDKAIYVLSAKRPLMLHMKRNP 840
 Db 862 KSDLHLPFCAMIFKNDLRODMVLVQYEVMDNITKAANIDCCLNPYAVLPGEMIGIT 921
 QY 841 KSDLHLPFCAMIFKNDLRODMVLVQYEVMDNITKAANIDCCLNPYAVLPGEMIGIT 900
 Db 922 EYVNPCKITFEIOVGTGFNNTAVRSIDPSFMNWKIRKOGIEDEKKSKSDSKNIEKK 981
 QY 901 EYVNPCKITFEIOVGTGFNNTAVRSIDPSFMNWKIRKOGIEDEKKSKSDSKNIEKK 960

Db 982 IDNTQAMKRESEVDRELYSCVGSVATYINGIKDRSHDNMLTDEGKYHIDFGHILGH 1041
 QY 961 IDNTQAMKRESEVDRELYSCVGSVATYINGIKDRSHDNMLTDEGKYHIDFGHILGH 1020
 Db 1042 GKTGKIGIORDRQPFILTFHEMTVIRSGKSVGNSHLOKFTLCVEANEVMMNRDLFVS 1101
 QY 1021 GKTGKIGIORDRQPFILTFHEMTVIRSGKSVGNSHLOKFTLCVEANEVMMNRDLFVS 1080
 Db 1102 LEFTLMGMEHPELSTKADLDHLKTLFCNGESKEARKFPAGIYEAFNGSMSTKNL 1161
 QY 1081 LEFTLMGMEHPELSTKADLDHLKTLFCNGESKEARKFPAGIYEAFNGSMSTKNL 1140
 Db 1162 HAVKH 1167
 QY 1141 HAVKH 1146

RESULT 2
 ID P11A_MOUSE STANDARD: PRT: 1068 AA.
 AC P42337;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM
 DE (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3-KINASE P110)
 DE (PI3K).
 GN PI3KA.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MORIDAE; MURINAE; MUS.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE: 94187738.
 RA Klippel A., ESCOBEDO J.A., HIRANO M., WILLIAMS L.T.;
 RT "The interaction of small domains between the subunits of
 RT phosphatidylinositol 3-kinase determines enzyme activity."
 RT MOL. CELL. BIOL. 14:2675-2685(1994).
 CC -1- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2 WITH A
 CC PREFERENCE FOR PTDINS(4,5)P2.
 CC -1- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-ID-MYO-INOSITOL -> ADP +
 CC 1-PHOSPHATIDYL-ID-MYO-INOSITOL 3-PHOSPHATE.
 CC -1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
 CC SUBUNIT.
 CC -1- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: U03279; G414995; -
 CC MGD: MGI:1206581; PI3KA.
 DR PROSITE: PS00915; PI3_A_KINASE_1; 1.
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 DR PROSITE: PS01172; PI3_A_KINASE_258; 1.
 DR PROSITE: PS01173; PI3_A_KINASE_259; 1.
 DR PROSITE: PS01174; PI3_A_KINASE_260; 1.
 DR PROSITE: PS01175; PI3_A_KINASE_261; 1.
 DR PROSITE: PS01176; PI3_A_KINASE_262; 1.
 DR PROSITE: PS01177; PI3_A_KINASE_263; 1.
 DR PROSITE: PS01178; PI3_A_KINASE_264; 1.
 DR PROSITE: PS01179; PI3_A_KINASE_265; 1.
 DR PROSITE: PS01180; PI3_A_KINASE_266; 1.
 DR PROSITE: PS01181; PI3_A_KINASE_267; 1.
 DR PROSITE: PS01182; PI3_A_KINASE_268; 1.
 DR PROSITE: PS01183; PI3_A_KINASE_269; 1.
 DR PROSITE: PS01184; PI3_A_KINASE_270; 1.
 DR PROSITE: PS01185; PI3_A_KINASE_271; 1.
 DR PROSITE: PS01186; PI3_A_KINASE_272; 1.
 DR PROSITE: PS01187; PI3_A_KINASE_273; 1.
 DR PROSITE: PS01188; PI3_A_KINASE_274; 1.
 DR PROSITE: PS01189; PI3_A_KINASE_275; 1.
 DR PROSITE: PS01190; PI3_A_KINASE_276; 1.
 DR PROSITE: PS01191; PI3_A_KINASE_277; 1.
 DR PROSITE: PS01192; PI3_A_KINASE_278; 1.
 DR PROSITE: PS01193; PI3_A_KINASE_279; 1.
 DR PROSITE: PS01194; PI3_A_KINASE_280; 1.
 DR PROSITE: PS01195; PI3_A_KINASE_281; 1.
 DR PROSITE: PS01196; PI3_A_KINASE_282; 1.
 DR PROSITE: PS01197; PI3_A_KINASE_283; 1.
 DR PROSITE: PS01198; PI3_A_KINASE_284; 1.
 DR PROSITE: PS01199; PI3_A_KINASE_285; 1.
 DR PROSITE: PS01200; PI3_A_KINASE_286; 1.
 DR PROSITE: PS01201; PI3_A_KINASE_287; 1.
 DR PROSITE: PS01202; PI3_A_KINASE_288; 1.
 DR PROSITE: PS01203; PI3_A_KINASE_289; 1.
 DR PROSITE: PS01204; PI3_A_KINASE_290; 1.
 DR PROSITE: PS01205; PI3_A_KINASE_291; 1.
 DR PROSITE: PS01206; PI3_A_KINASE_292; 1.
 DR PROSITE: PS01207; PI3_A_KINASE_293; 1.
 DR PROSITE: PS01208; PI3_A_KINASE_294; 1.
 DR PROSITE: PS01209; PI3_A_KINASE_295; 1.
 DR PROSITE: PS01210; PI3_A_KINASE_296; 1.
 DR PROSITE: PS01211; PI3_A_KINASE_297; 1.
 DR PROSITE: PS01212; PI3_A_KINASE_298; 1.
 DR PROSITE: PS01213; PI3_A_KINASE_299; 1.
 DR PROSITE: PS01214; PI3_A_KINASE_300; 1.
 DR PROSITE: PS01215; PI3_A_KINASE_301; 1.
 DR PROSITE: PS01216; PI3_A_KINASE_302; 1.
 DR PROSITE: PS01217; PI3_A_KINASE_303; 1.
 DR PROSITE: PS01218; PI3_A_KINASE_304; 1.
 DR PROSITE: PS01219; PI3_A_KINASE_305; 1.
 DR PROSITE: PS01220; PI3_A_KINASE_306; 1.
 DR PROSITE: PS01221; PI3_A_KINASE_307; 1.
 DR PROSITE: PS01222; PI3_A_KINASE_308; 1.
 DR PROSITE: PS01223; PI3_A_KINASE_309; 1.
 DR PROSITE: PS01224; PI3_A_KINASE_310; 1.
 DR PROSITE: PS01225; PI3_A_KINASE_311; 1.
 DR PROSITE: PS01226; PI3_A_KINASE_312; 1.
 DR PROSITE: PS01227; PI3_A_KINASE_313; 1.
 DR PROSITE: PS01228; PI3_A_KINASE_314; 1.
 DR PROSITE: PS01229; PI3_A_KINASE_315; 1.
 DR PROSITE: PS01230; PI3_A_KINASE_316; 1.
 DR PROSITE: PS01231; PI3_A_KINASE_317; 1.
 DR PROSITE: PS01232; PI3_A_KINASE_318; 1.
 DR PROSITE: PS01233; PI3_A_KINASE_319; 1.
 DR PROSITE: PS01234; PI3_A_KINASE_320; 1.
 DR PROSITE: PS01235; PI3_A_KINASE_321; 1.
 DR PROSITE: PS01236; PI3_A_KINASE_322; 1.
 DR PROSITE: PS01237; PI3_A_KINASE_323; 1.
 DR PROSITE: PS01238; PI3_A_KINASE_324; 1.
 DR PROSITE: PS01239; PI3_A_KINASE_325; 1.

Db 326 SLWVNSALRIK-ILCATYVNNIRIDIKIYRT--GIYHGEPICDNVNTORPCSNR 382
 QY 385 SLWMDLANMIRVNIISGF-DEPA-DVD-MYRIEFSYVGLTLASK-STKVNQAFK 440
 Db 383 WN-EMLVNDIYIPDLPRARLCLISGVGRKGAKEHCPLAMGNINLFDYDTLVSGKM 441
 QY 441 WNKEMTFEFLYKMDMPSA-V-LSTRVLGYKYLKSEEFEGVMVNSLTDMDRDLROGOF 498
 Db 442 ALNIMPVPHGLEDLNPIVGTGNSPNKTEPCLEFDMFSSVVKPDMVIEEHANWSVS 501
 QY 499 LFHLM-PEPTANR-SRIENGARIGTNA-VTIEISYGRVMP--S--OGYTTLV 550
 Db 502 RENGEFSYSHAGLSNRLARDNE-LRENDKEQLRAICTRDLSETTEOEKD-FLMSHRHYC 558
 QY 551 KHRN-TWET-L-NIMDDDESCIRDPGYKRLQMLVKKHESGIYLEDDEQHNMMRYI 607
 Db 559 VT-IPETLPRLL-LSVKNNSDEVAQMYCLYKMPPIKPEQAMLLDONTDPVRSFAY 616
 QY 608 OKOEPDLIYSELAFYWTDEENSELYVMLEKKRPPSVAALLTLGKRCIDRVIRKFAV 667
 Db 617 RCEKYTLDDKLSQYLQVQVLYKEYOYLDNLVRLFKKALTNQRIQGHFFHMLKSE-- 674
 QY 668 EKLINEQSPVTFHFLIPLIALKTEBPRAQSEVGMMLTLRALCDYRIGHRLFWLRAEIA 727
 Db 675 -MHN---KTVS-QRFGLLSEYACAGMYLKLHNOYEAAMEKLINTDLIKOEKKDETOK 729
 QY 728 RLRCODKSEERYRISLMEAYLNGNEHKKIITROYDMDELRISTLVKGMKDYA-- 785
 Db 730 VOMKFLVEOROPDFMDALOGFLSPINPAHOLGNLRECRINSASARPLIMNENDIM 789
 QY 786 T-WK-LDELR-S-ISKKNMNSPDPYKLGEMITDKALVLSASARPLMLHKNKNPK 841
 Db 790 SELFONNEIFKNGDRLKODMLTLQIRIMENINQOGLDRLMPLGCLSIGDCVGLIE 849
 QY 842 SDHLPEFCAMIFKNGDRLKODMLVLYLEVMDNIMKANIIDCCNPAVAVPMGMIGITIE 901
 Db 850 VVNSHTIMIOCKG-LKALQ-FNSHTIHOWL-K-----D-KNGC-ETV-DA-A--1 894
 QY 902 VVPRCKTIFEIYGTGEMTNAVSIDSFNNKWIIRKOCGIEDEKSKKSTKNPIEKKI 961
 Db 895 D-----F-T---R---SCAGYCVATFIIIGDRHNSNIMVDDGOLFIDHGHFLDK 941
 QY 962 DNGQAKKKYESVDRLYSCVGSVATYINGIDRHSNMLNLEDGYVIAIDGHILGHG 1021
 Db 942 KKKFGKREVPVLTODFLIVISKAQETKTRFEFQEMCYKAVLAIRHANFINTL 1001
 QY 1022 KTLGIOROROPILTEHEFTVIRSGKSVGNSHLOKFKTLCEAVEYVMNNRDLFVSL 1081
 Db 1002 FSNMISGMELOSFDIAYIRKTL-ALDKTEQEALEYFKKONNDANHGVTWKMDWIFH 1060
 QY 1082 FTLMLEDELSTKADLHLKTLKFCNGESKEEARFAGIYEAFNGSMSTKTNWLFH 1141
 Db 1061 TIRQ 1064
 QY 1142 AVKH 1145
 RESULT 3
 ID P11A-BOVIN STANDARD; PRT; 1068 AA.
 AC P32871;
 DT 01-OCT-1993 (REL. 27, LAST CREATED)
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM
 (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3-KINASE P110)
 DE (PI3K).
 GN PI3KA.
 OS BOS TAURUS (BOVINE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLIA; RUMINANTIA; PECORA; BOVOIDEA; BOVINAE; BOS.
 RN (1)
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE-BRAIN;
 RX MEDLINE; 92354059.
 RA FILES I.D., OTSU M., VOLINIA S., FRY M.J., GOUT I., DHAND R.,
 RA PANAYOTOV G., RUIZ-IBARRA F., THOMPSON A., TOTTY N.F., HSUAN J.J.,
 RA COURTNEIDGE S.A., PARKER P.J., WATERFIELD M.D.,
 RT "phosphatidylinositol 3-kinase: structure and expression of the 110
 RT Kd catalytic subunit.";
 RL CELL 70:419-429(1992).
 CC -1- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2 WITH A
 CC PREFERENCE FOR PTDINS(4,5)P2.
 CC -1- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL - ADP +
 CC 1-PHOSPHATIDYL-1D-MYO-INOSITOL 3-PHOSPHATE.
 CC -1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
 CC SUBUNIT.
 CC -1- SIMILARITY: BELONGS TO THE PI3/P14-KINASES FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC
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 CC
 DR EMBL; M93252; G163520; -.
 DR PIR; A43322; A43322.
 DR PROSITE; PS00915; PI3_4_KINASE_1; 1.
 DR PROSITE; PS00916; PI3_4_KINASE_2; 1.
 DR PROSITE; PS00916; PI3_4_KINASE_2; 1.
 DR PROSITE; PS00916; PI3_4_KINASE_2; 1.
 DR PFAM; PF00454; PI3_DOMAIN_2; FALSE_NEG.
 DR PFAM; PF00613; PI3K; 1.
 DR PFAM; PF00792; PI3K_C2; 1.
 DR PFAM; PF00794; PI3K_C2; 1.
 DR TRANSFERASE; KINASE; MULTIGENE FAMILY.
 FT DOMAIN 319 428
 FT C2 DOMAIN.
 FT P13K/PI3K.
 FT DOMAIN 799 1053
 FT SEQUENCE 1068 AA; 124327 MW; 69160287 CRC32;
 Query Match 13.4%; Score 1151; DB 1; Length 1068;
 Best Local Similarity 30.7%; Pred. No. 5.28e-223;
 Matches 240; Conservative 212; Mismatches 266; Indels 64; Gaps 41;
 Db 326 SLWVNSALRIK-ILCATYVNNIRIDIKIYRT--GIYHGEPICDNVNTORPCSNR 382
 QY 385 SLWMDLANMIRVNIISGF-DEPA-DVD-MYRIEFSYVGLTLASK-STKVNQAFK 440
 Db 383 WN-EMLVNDIYIPDLPRARLCLISGVGRKGAKEHCPLAMGNINLFDYDTLVSGKM 441
 QY 441 WNKEMTFEFLYKMDMPSA-V-LSTRVLGYKYLKSEEFEGVMVNSLTDMDRDLROGOF 498
 Db 442 ALNIMPVPHGLEDLNPIVGTGNSPNKTEPCLEFDMFSSVVKPDMVIEEHANWSVS 501
 QY 499 LFHLM-PEPTANR-SRIENGARIGTNA-VTIEISYGRVMP--S--OGYTTLV 550
 Db 502 RENGEFSYSHAGLSNRLARDNE-LRENDKEQLRAICTRDLSETTEOEKD-FLMSHRHYC 558
 QY 551 KHRN-TWET-L-NIMDDDESCIRDPGYKRLQMLVKKHESGIYLEDDEQHNMMRYI 607
 Db 559 VT-IPETLPRLL-LSVKNNSDEVAQMYCLYKMPPIKPEQAMLLDONTDPVRSFAY 616
 QY 608 OKOEPDLIYSELAFYWTDEENSELYVMLEKKRPPSVAALLTLGKRCIDRVIRKFAV 667
 Db 617 RCEKYTLDDKLSQYLQVQVLYKEYOYLDNLVRLFKKALTNQRIQGHFFHMLKSE-- 674
 QY 668 EKLINEQSPVTFHFLIPLIALKTEBPRAQSEVGMMLTLRALCDYRIGHRLFWLRAEIA 727
 Db 675 -MHN---KTVS-QRFGLLSEYACAGMYLKLHNOYEAAMEKLINTDLIKOEKKDETOK 729
 QY 728 RLRCODKSEERYRISLMEAYLNGNEHKKIITROYDMDELRISTLVKGMKDYA-- 785
 Db 730 VOMKFLVEOROPDFMDALOGFLSPINPAHOLGNLRECRINSASARPLIMNENDIM 789
 QY 786 T-WK-LDELR-S-ISKKNMNSPDPYKLGEMITDKALVLSASARPLMLHKNKNPK 841
 Db 790 SELFONNEIFKNGDRLKODMLTLQIRIMENINQOGLDRLMPLGCLSIGDCVGLIE 849
 QY 842 SDHLPEFCAMIFKNGDRLKODMLVLYLEVMDNIMKANIIDCCNPAVAVPMGMIGITIE 901
 Db 850 VVNSHTIMIOCKG-LKALQ-FNSHTIHOWL-K-----D-KNGC-ETV-DA-A--1 894
 QY 902 VVPRCKTIFEIYGTGEMTNAVSIDSFNNKWIIRKOCGIEDEKSKKSTKNPIEKKI 961
 Db 895 D-----F-T---R---SCAGYCVATFIIIGDRHNSNIMVDDGOLFIDHGHFLDK 941
 QY 962 DNGQAKKKYESVDRLYSCVGSVATYINGIDRHSNMLNLEDGYVIAIDGHILGHG 1021
 Db 942 KKKFGKREVPVLTODFLIVISKAQETKTRFEFQEMCYKAVLAIRHANFINTL 1001
 QY 1022 KTLGIOROROPILTEHEFTVIRSGKSVGNSHLOKFKTLCEAVEYVMNNRDLFVSL 1081
 Db 1002 FSNMISGMELOSFDIAYIRKTL-ALDKTEQEALEYFKKONNDANHGVTWKMDWIFH 1060
 QY 1082 FTLMLEDELSTKADLHLKTLKFCNGESKEEARFAGIYEAFNGSMSTKTNWLFH 1141
 Db 1061 TIRQ 1064
 QY 1142 AVKH 1145
 RESULT 3
 ID P11A-BOVIN STANDARD; PRT; 1068 AA.
 AC P32871;
 DT 01-OCT-1993 (REL. 27, LAST CREATED)
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM
 (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3-KINASE P110)
 DE (PI3K).
 GN PI3KA.
 OS BOS TAURUS (BOVINE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLIA; RUMINANTIA; PECORA; BOVOIDEA; BOVINAE; BOS.
 RN (1)
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

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OY 787 MK-LBDEL-R-S-ISHKEMNDSPDPVYKLGEMIIDKALVGSARRPLMLANKNPKSD 843
DB 792 LIFONNEIFKNGDDLRQDMLTQIRIMENIMONOGDLRLPYGCLSIDGVLIEV 851
OY 844 LHLPCAMIFKNGDDLRQDMLTQVLEVDNIMKANAIDCCNPAVAVPMGEMIGIEV 903
DB 852 RNSHTIMOQCKG-LKALQ-FNSHTLHOWL-K-----D-KNG--EIV-DA-A-ID- 895
OY 904 PCKTIFEFVGTGFPMNVAIRSIDPSFNKWKIRKOCGIEDEKSKSKSTKPIEKKIDN 963
DB 896 ---L--F-T--R---SCAGCVATFIIIGIGRHSNINMVKDQGLFHDGPHDHHK 943
OY 964 TQAMKRYESVDRFLYSCGVSVATYIMGIKDRHSNDMLTDEGKYVHIDFGHILGHKT 1023
DB 944 KFGYKREVPVLTODFLIVISKGAOECKTRERFERFOMCYKAYLAIRQHANLFINFS 1003
OY 1024 KIGIQDRQPFILTEHFVIVIRSGKSVDSNHELQKFKLCYEALEVMMNNNDLVSFLT 1083
DB 1004 KMLGSGMPELQSFDDIAYIRKTL-ALDKTEQALEYFKOMNDHGHGTTKMDIETFTI 1062
OY 1084 LMLGMLPELSTKADLDHDKTLFCNGESKEBARKFAGIYEAFNGSVSTKTNLFAV 1143
DB 1063 KQ 1064
OY 1144 KH 1145

RESULT 4
ID P11A HUMAN STANDARD: PRT: 1068 AA.
AC P42336: Q99762:
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM
  (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3-KINASE P110)
DE (PI3K).
GN PI3KA.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RX MEDLINE: 95229146.
RA VOLINIA S., HILES I., ORMONDROYD E., NIZETIC D., ANTONACCI R.,
RA ROCCHI M., WATERFIELD M.;
RT "Molecular cloning, cDNA sequence, and chromosomal localization of
  the human phosphatidylinositol 3-kinase p110 alpha (PIK3CA) gene.";
RL GENOMICS 24:472-477(1994).
RN [2]
RN SEQUENCE FROM N.A.
RA STIRDIVANT S.M., AHERN J., CONROY R.R., BARNETT S.F., LEDDER L.M.,
RA OLIVER A., HEIMBROOK D.C.;
RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC -1- FUNCTION: PHOSPHORYLATES PTDINS, PTDINSAP AND PTDINS(4,5)P2.
CC PREFERENCE FOR PTDINS(4,5)P2.
CC -1- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL = ADP +
CC 1-PHOSPHATIDYL-1D-MYO-INOSITOL 3-PHOSPHATE.
CC -1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
CC SUBUNIT.
CC -1- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -----
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CC -----
DR EMBL: Z29090: G472991: -
DR EMBL: U79143: G1763626: -
DR MTM: 171834: -

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DR PROSITE; PS00915; PI3_4_KINASE.1; 1.
DR PROSITE; PS00916; PI3_4_KINASE.2; 1.
DR PROSITE; PS50004; C2_DOMAIN.2; FALSE_NG.
DR PFAM; PF00454; PI3_P14_kinase; 1.
DR PFAM; PF00613; PI3Ka; 1.
DR PFAM; PF00792; PI3K_C2; 1.
DR PFAM; PF00794; PI3K_Ltdb; 1.
DR PFAM; PF00794; PI3K_Ltdb; 1.
DR TRANSFERASE; KINASE; MULTIGENE FAMILY.
FT DOMAIN 319 428
FT C2_DOMAIN
FT P13K/PI4K
FT CONFLICT 43 1053
FT CONFLICT 170 170
FT CONFLICT 170 170
FT CONFLICT 187 187
FT CONFLICT 286 287
FT CONFLICT 332 332
FT CONFLICT 332 332
FT CONFLICT 346 346
FT CONFLICT 723 723
FT CONFLICT 751 751
FT CONFLICT 767 767
FT CONFLICT 767 767
SQ SEQUENCE 1068 AA; 124412 MW; 5890D04A CRC32;

Query Match 13.4%; Score 1151; DB 1; Length 1068;
Best Local Similarity 30.7%; Pred. No. 5,286-223;
Matches 240; Conservative 211; Mismatches 267; Indels 64; Gaps 41;

DB 326 SLWVNRALRIK-IICATVYMLNTRDIDKIYRT--GIYHGEPFLCDNVNTQVPCSNPR 382
OY 385 SLMDLDANLMIRPVNISGF-DEPA-DVD-MYVRIEFVYVGTLLTASK-STTKVNAQFAK 440
DB 383 WN-EWLANDIYTPDPRARCLSTCSYKGRKKEHCPLAMGNINLFDVTDLVSGKM 441
OY 441 WKREYTYTDLWKMDPPA-V-LSTRVLYGVKLSKEFEFEGVGNMSTLTDRELDROQF 498
DB 442 ALNLPVPHGEDLLDLPPIATVGSNPNKETPCLEFEFSSVYVFXPDMSVIEHANMSVS 501
OY 442 ALNLPVPHGEDLLDLPPIATVGSNPNKETPCLEFEFSSVYVFXPDMSVIEHANMSVS 501
DB 499 LEHMA-PEPTANR-SRIGENGARIGTMA-VTIEISSGGRVMP--S-QGQYTLVK 551
OY 499 LEHMA-PEPTANR-SRIGENGARIGTMA-VTIEISSGGRVMP--S-QGQYTLVK 551
DB 502 REAGESYHAGISNRLANDNDELRENDKQALKAISTROPDLSITDOEK-FLMSHRHCYT 560
OY 502 REAGESYHAGISNRLANDNDELRENDKQALKAISTROPDLSITDOEK-FLMSHRHCYT 560
DB 552 HRSWTETLIMGDDY--ESCIKDPGKYLQMLVKKHESGIVLEDEQRYHVMNRRTYOK 609
OY 552 HRSWTETLIMGDDY--ESCIKDPGKYLQMLVKKHESGIVLEDEQRYHVMNRRTYOK 609
DB 561 -IPELIPKLL-LSVKNRSDEVAQMYCYKMDPPKIPQANELLDCNPDPMVGEFAVC 618
OY 610 QEPDILLIVSELAFTWDTRENSELYVLEKMKPPSAVALTLGKCTDVIKFAVEK 669
DB 619 LEKYITDKLSQYLQVLYQVLYQVLYQVLYQVLYQVLYQVLYQVLYQVLYQVLYQVLYQV 675
OY 670 LNEQLSPVTFHFLIPLOALKTEPRAQSEVMMLTRALDQYRIGRHLFWLREIARL 729
DB 676 HN---KTVS-QRFGLLSYCRACGMYKHLNROYEAMEKILNTDILKQERKDETQVQ 731
OY 676 HN---KTVS-QRFGLLSYCRACGMYKHLNROYEAMEKILNTDILKQERKDETQVQ 731
DB 730 RDCDCKSEERYRISILMAEYLNENHETITROYDVEDLTRISTLVKGPKQVA--T- 786
OY 730 RDCDCKSEERYRISILMAEYLNENHETITROYDVEDLTRISTLVKGPKQVA--T- 786
DB 733 MKEIVQMRPDMFQALGGLSPNPAHQGLRLKECRINSSAKRPLMLMNNPDINSE 791
OY 787 MK-LBDEL-R-S-ISHKEMNDSPDPVYKLGEMIIDKALVGSARRPLMLANKNPKSD 843
DB 792 LIFONNEIFKNGDDLRQDMLTQIRIMENIMONOGDLRLPYGCLSIDGVLIEV 851
OY 844 LHLPCAMIFKNGDDLRQDMLTQVLEVDNIMKANAIDCCNPAVAVPMGEMIGIEV 903
DB 852 RNSHTIMOQCKG-LKALQ-FNSHTLHOWL-K-----D-KNG--EIV-DA-A-ID- 895
OY 904 PCKTIFEFVGTGFPMNVAIRSIDPSFNKWKIRKOCGIEDEKSKSKSTKPIEKKIDN 963
DB 896 ---L--F-T--R---SCAGCVATFIIIGIGRHSNINMVKDQGLFHDGPHDHHK 943
OY 964 TQAMKRYESVDRFLYSCGVSVATYIMGIKDRHSNDMLTDEGKYVHIDFGHILGHKT 1023
DB 944 KFGYKREVPVLTODFLIVISKGAOECKTRERFERFOMCYKAYLAIRQHANLFINFS 1003
OY 1024 KIGIQDRQPFILTEHFVIVIRSGKSVDSNHELQKFKLCYEALEVMMNNNDLVSFLT 1083

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Db 1004 MMLGSGPELQSFDDIYIRKTL-ALDKTEBALEFPMKQNDNAHGCWTMIFHTI 1062
 QY 1084 LMGMEPELSTKADLHLKTKLFCEGSKSEKARFAGIYEAFNGSWSTKTMWLFHAV 1143
 Db 1063 KQ 1064
 QY 1144 KH 1145

RESULT 5
 ID P1LB-HUMAN STANDARD; PRT; 1070 AA.
 AC P42338;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE PHOSPHATIDYL-INOSITOL 3-KINASE CATALYTIC SUBUNIT, BETA ISOFORM
 DE (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT BETA) (PTDINS-3-KINASE P110)
 DE (PI3K).
 GN PI3KB.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94067128.
 RA HD P., MONDINO A., SKOLNIK E.Y., SCHLESSINGER J.;
 RT Cloning of a novel, ubiquitously expressed human
 RT phosphatidylinositol 3-kinase and identification of its blinding site
 RT on p85.".
 RL MOL. CELL. BIOL. 13:7677-7688(1993).
 CC -1- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2 WITH A
 CC PREFERENCE FOR PTDINS(4,5)P2.
 CC -1- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-ID-MYO-INOSITOL = ADP +
 CC 1-PHOSPHATIDYL-ID-MYO-INOSITOL 3-PHOSPHATE.
 CC -1- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.
 CC -1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
 CC SUBUNIT.
 CC -1- TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.
 CC -1- SIMILARITY: BELONGS TO THE PI3/P14-KINASES FAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: S67334; G455760; .
 DR MIM; 602923; .
 DR PROSITE; PS00915; PI3_4_KINASE.1; 1.
 DR PROSITE; PS00916; PI3_4_KINASE.2; 1.
 DR PRAM; PF00454; PI3_P14_kinase; 1.
 DR PRAM; PF00613; PI3ka; 1.
 DR PRAM; PF00792; PI3K_C2; 1.
 DR PRAM; PF00794; PI3K_Tcd; 1.
 DR TRANSFERASE; KINASE; MULTIGENE FAMILY.
 KW DOMAIN 802 1055 PI3K/PIAK.
 FT SEQUENCE 1070 AA; 122762 MW; 89AA20DF CRC32;
 SO

Query Match 11.7%; Score 1011; DB 1; Length 1070;
 Best Local Similarity 34.1%; Pred. No. 1,20e-190;
 Matches 233; Conservative 170; Mismatches 217; Indels 63; Gaps 43;

Db 436 YPVAVNTVWDFGKGRGTGDIILHSWSPFDELEMLNPGT-VQNP-YT-ENAT-AL 491
 QY 477 FENGWVNSLTDWDELROGOFELHWAPEFTANRSRIGENGARIGTAAVITISISGG 536
 Db 492 HVKPEPKKOPYPPDKII-EKAAEIASDSAN-VSSRGSKFLPYLKEIIRDPISQ 549
 QY 537 RVRNP-SOGQ-YTLVVKHRSWTETLNMGDYESCIRDPYK-LQML-VKHHESGIV 591
 Db 550 LCEHEMLITLRODCREIFPQSLKILL-ISIKNNKLEDAVQAQALQIWEKLP-REAL 607

QY 592 LEEDEQRHVMWRRYIQKQEPDLILVLELAFWTDRENSELYVMLEK-KPESVAAL 650
 Db 608 ELDFENPDQVREYAVGCLR-QMSDELSOYLQLOVYKREPFELCALSRFLLEALG 666
 QY 651 TLGKRTDRIYKFAVEKLENEQSPYTHFLFIPLIQAKEYEPRAOSEVGMILLTALC 710
 Db 667 NRRIGOLFVHLRSEV-HIPA-V-SVOFG-V-IL-EAYCGSGVGHKKVLSKOYEALNKL 719
 QY 711 DYRIGRLFWLRAEIRARLDCLDKSEYRISILMEAYLRNGNEHIKITRQVDWDEL 770
 Db 720 KTLNSLIKLAVALNRAKGEAMHTCLKQSAKREALSDLOSPNLCYILSELYVEKRYM 779
 QY 771 TRISTLVK-GMPK-DVATMK--LDELRSISHK--MENKSDPLDPYKLGEMITDKAIVL 824
 Db 780 DSKKRPMLVYNNKVF-GE-D-SV-GVIFKNGDGLRDMTLQMLRLMDLWKEAGDLR 835
 QY 825 GSAKRPMLMKKKNPKSDHLFPCAMIFKNGDDLRQDMVLVQLEVMNIMKRAIDCC 884
 Db 836 MLPYGLATGDRGLIEVASTSETIADIQNSSNVAAMAAFNKDALLN-WL-KEY--NS 890
 QY 885 LNPYAVLPMGEMIGIIEVNPCKTIFEIQVGTGMNTAVSIDSFNNKWIIRKQGIIDE 944
 Db 891 ---G-D---D-LDRAIE--E-----F-T---L-SCAGCVASYVIGIDRRSDNIMK 928
 QY 945 KKSKKDSKTNPKLEKIDNTQAMKYESVDRELFVSCVGSVAIYINGIDRRSDNIMLT 1004
 Db 929 KTGOLFIDFGHILGNFKSGFKREKREVPFLIYDFHVIQOOGKT--GNTKGRFRQCC 986
 QY 1005 EDGKYVIDGHILGHOKRTKLGIDRORPILIEHFTVIRSGKSDGNSHELOKFTLC 1064
 Db 987 EDAYILRRGNFTFLFALMTAGLELTSYVDIYQIKLSD-ALGKSEBALKQFROKF 1045
 QY 1065 VEAVEVWNNRDLFVSLFTLMIGMEPELSTKADLHLKTKLFCEGSKSEKARFAGIY 1124
 Db 1046 DEALRESWTIKVMAMTAVKDY 1068
 QY 1125 EEAENGSMSTKTMWLFHAV-KHY 1146

RESULT 6
 ID P11G-PIG STANDARD; PRT; 1102 AA.
 AC 002697;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE PHOSPHATIDYL-INOSITOL 3-KINASE CATALYTIC SUBUNIT, GAMMA ISOFORM
 DE (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT GAMMA) (PTDINS-3-KINASE P110)
 DE (PI3K) (P120-PI3K).
 GN PI3CG.
 OS SUS SCROFA (PIG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RP TISSUE-NEUTROPHILS;
 RX MEDLINE: 97248491.
 RA STEPHENS L.R., EGUINOA A., ERDJUMENT-BRONAGE H., LUI M., COOKE F.,
 RA COWDELL J., SNAKCA A.S., THELEN M., CADWALLADER K., TEMPEST P.,
 RA HAWKINS P.T.;
 RT The gamma kinase sensitivity of a PI3K is dependent upon a tightly
 RT associated adaptor, p101.";
 RL CELL 89:105-114(1997).
 RN [2]
 RP REVISIONS.
 RA STEPHENS L.R.;
 RL SUBMITTED (APR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: 3-PHOSPHORYLATES THE CELLULAR PHOSPHOINOSITIDE
 CC PTDINS-4,5-BIPHOSPHATE (PTDINS(4,5)P2).
 CC -1- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-ID-MYO-INOSITOL = ADP +
 CC 1-PHOSPHATIDYL-ID-MYO-INOSITOL 3-PHOSPHATE.
 CC -1- SUBUNIT: HETERODIMER OF A 101 KD SUBUNIT AND A 120 KD CATALYTIC
 CC SUBUNIT.


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OY 706 TRALCYRICHRLFPALLRAIALRBOCDLSEERYRSLTMEYLYKNEHIIITROYD 765
DB 687 ALSKALNDFYVSSOKTTPQTKEMHMCROETYMALSHLOSLPSTLEECVCE 746
OY 766 MDELTRISTLYV-GMPKIDV-A-TMKLRDE-LKSISHK--MEMNDSPDPVYLGEMIID 819
DB 747 QCFPMDSKKPLIMVSSSEAGSAGV---GIFKMGDDLRQMLTLOMTLOMDVLMKOE 803
OY 820 KATVLSARPLMLHMKNNPKSDHLPCFCAMIFKNGDDLRQMLVQYLEVANDNIMKAA 879
DB 804 GLDLRATPYGLTGDRTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLTGLT 852
OY 880 NIDCCNPAVAVLPMGEMIGIEVVPCKITFELQVGTGFMNIVRSIDSEFNKKIRKOC 939
DB 853 ALIN-WLCK-NPG-EALDRAIE-E-----F-T-----L-SCAGCVATVYLGIDRHS 896
OY 940 GIEDEKSKKSKSTKNPKIDNTQAMKVFESYDRFLYSCVSVATYIMKIDRHS 999
DB 897 NIMIRSSGLFHDGFIHGFNGFTKFCINRERPFILITDFVAVIOGKT-N-NSEKFER 954
OY 1000 NMLTLDGQYVYHDFHGLHGHGKTGLGIQDRQPFILTEHFMVIVISGKSVDSNHELQK 1059
DB 955 FPGYCEATYILRRGLFLFLHFAALRAAGLPETSCSDIOYLDKSL-ALGKEEALKH 1013
OY 1060 FTLCVEAEVVMNNNDLVSLFTLMLGHELPSTKADLDLKTFLCNGESKEARKE 1119
DB 1014 FVKEALRESKTKVNNLANVY 1037
OY 1120 FAGIYEAEFGSWSTKTNMLFHAV 1143

RESULT 8
ID P11G-HUMAN STANDARD: PRT: 1101 AA.
AC P48736:
DB 01-FEB-1996 (REL. 33, CREATED)
DB 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DB 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE PHOSPHATIDYL-INOSITOL 3-KINASE CATALYTIC SUBUNIT, GAMMA ISOFORM
DE (EC 2.7.1.137) (P13-KINASE P110 SUBUNIT GAMMA) (P1DINS-3-KINASE P110)
DE (P13K).
GN PIR3CG.
OS HOMO SAPIENS (HUMAN).
OC EURARYOTA: MEZAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA.
OC PRIMATES: CARARRINI: HOMINIDAE: HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95350661.
RA STOVANOV B., VOLINIA S., HANCK T., RUBIO I., LOUBCHENKOV M.,
RA MALEK D., STOVANOVA S., VANHASEBOECK B., DHAND R., NUERNBERG B.,
RA GIRSCHIK P., SEDORF K., HSUAN J.J., WATERFIELD M.D., WETZLER R.,
RT "Cloning and characterization of a G protein-activated human
RT phosphoinositide-3 kinase."
RT SCIENCE 269:690-693(1995).
RL [2]
RN REVISIONS.
RP WATERFIELD M.D.:
RA SUBMITTED (AUG-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: 3-PHOSPHORYLATES THE CELLULAR PHOSPHOINOSITIDE
CC P1DINS-4,5-BIPHOSPHATE (P1DINS(4,5)P2).
CC -1- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-ID-MYO-INOSITOL - ADP +
CC 1-PHOSPHATIDYL-ID-MYO-INOSITOL 3-PHOSPHATE.
CC -1- ENZYME REGULATION: ACTIVATED BY BOTH THE ALPHA AND THE BETA-GAMMA
CC G PROTEINS.
CC -1- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.
CC -1- SUBUNIT: HETERODIMER OF A 101 KD SUBUNIT AND A 120 KD CATALYTIC
CC SUBUNIT (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PANCREAS, SKELETAL MUSCLE, LIVER, AND HEART.
CC -1- SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.
CC -----
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CC -----
DB EMBL: X83368; E264520; -
DR MIM: 601232; -
DR PROSITE: PS00915; P13_4_KINASE.1; 1.
DR PROSITE: PS00916; P13_4_KINASE.2; 1.
DR PFAM: PF00454; P13_P14_Kinase; 1.
DR PFAM: PF00613; P13Ka; 1.
DR PFAM: PF00792; P13K_C2; 1.
DR PFAM: PF00794; P13K_Ibd; 1.
DR TRANSFERASE: KINASE: MULTIGENE FAMILY.
KW DOMAIN 829 1074 P13K/P14K.
SO SEQUENCE 1101 AA; 126410 MW; 1296011AD CRC32:

Query Match 11.28; Score 961; DB 1; Length 1101;
Best Local Similarity 32.8%; Pred. No. 3,78e-179;
Matches 222; Conservative 176; Mismatches 216; Indels 62; Gaps 31;

DB 463 VMLLIDHRLRGRGYVLMHMOISGKE-DGSPNADKLTSATNPDK-NSMSTISILD 520
OY 482 VMSLSLDMWDELROGQFELHWAPEPTANRSRIENGARIGNAVTEISSYGRVMP 541
DB 521 NYCHPLALPKHOPT-PDP-E--GDRVRAEMPQOLRKOLEAITAT-DPLNPLAEDKELM 575
OY 542 SGGQYTLVYKHSSTWETINIMGGDYESCIRDPGRKLOMLYKHEGVLDEDEORHW 601
DB 576 HRR-YESLKHPRAYKLS-SYKMGQOETVANTYOLLARREVDOSALDVGTLMDLON 633
OY 602 MWRRIYOKOEPDLILVLSLAFWTDRENFSELYMLEK--WKPPSVAALT--LLGR 656
DB 634 FSDENVRALVOKLESLEDDVLH-YLLOVQAVKFEPPYHDSALRFLKRLKRRIGH 692
OY 657 CTDRYIRKFAVEKLEQUSPVTEHFLPLIOLALYEPPOSEVEMMLTRALCYRIGH 716
DB 693 FLEWFLRSEIAOSRYH---QQ--RFAVILEAYLRGCGTAMHDPTQOVVEMLOKYL 746
OY 717 RLFWLLRAEIALRBOCDLSEERYRSLTMEYLYKNEHIIITROYDDELTRIST 775
DB 747 DIKLSAEKIVYSSOVISOLKOLENLSNOLPESFRVYPDGLAGALATECKVMASK 806
OY 776 LVKGP--K-DVAT--M-KLRDELRSISH-KM-ENMDSPLDPVYKLGEMIIDKALVLSA 827
DB 807 KKPWLFEKADPTA-LSNETIGIFKFGDULRQMLLQIIRIMESIWESLDCILP 865
OY 828 KNPDLHMKNNPKSDHLPCFCAMIFKNGDDLRQMLVQYLEVANDNIMKANIDCCNLP 887
DB 866 YGCISTDGKIGMIEIVKDATYIAKIOOSTV-GNTG-AFKDEVLHML-K-----EK-- 913
OY 888 YAVLPMGEMIGIEVVPCKITFELQVGTGFMNIVRSIDSEFNKKIRKOCGIDEXKK 947
DB 914 -----S-----PTEBEK--OA-----AVERVYSCAGCVATVYLGIDRHNINWITETG 957
OY 948 SKDSTKNPKIDNTQAMKVFESYDRFLYSCVSVATYIMKIDRHSNMLTLEDG 1007
DB 958 NLEHIDFGHILGNVSEFINKERPFVLPDLEFVM--GISGKTSHPQKODICVKA 1015
OY 1008 KYVHIDFHHILGHGKTGLGIQDRQPFILTEHFMVIVISGKSVDSNHELQKFLCVEA 1067
DB 1016 YLALRHNTLLILFESMLMTGMPOLSKEDIEYTRDAL-TVGNKEEDAKRYFYLDQIEVC 1074
OY 1068 YEVMNNNDLVSLFTLMLGHELPSTKADLDLKTFLCNGESKEARKEFFAGIYEEA 1127
DB 1075 RDKGTVQFNNFHLVY 1090
OY 1128 FNGSWSTKTNMLFHAV 1143

RESULT 9
ID P11D HUMAN STANDARD: PRT: 1044 AA.
AC O00329; O15445;

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DR PFAM: PF00454; P13, P14, Kinase: 1.
 DR PFAM: PF00613; P13Ka, 1.
 DR PFAM: PF00792; P13K_C2: 1.
 DR PFAM: PF00794; P13K_Ibd: 1.
 KW TRANSFERASE: KINASE; MULTIGENE FAMILY.
 FT DOMAIN 34 40 POLY-GLY.
 FT DOMAIN 166 172 POLY-SER.
 FT DOMAIN 185 226 POLY-ASN.
 FT DOMAIN 227 235 POLY-THR.
 FT DOMAIN 246 253 POLY-SER.
 FT DOMAIN 259 268 POLY-ASN.
 FT DOMAIN 294 303 POLY-THR.
 FT DOMAIN 361 364 POLY-SER.
 FT DOMAIN 369 384 POLY-SER.
 FT DOMAIN 423 429 POLY-GLN.
 FT DOMAIN 439 444 POLY-THR.
 FT DOMAIN 445 454 POLY-SER.
 FT DOMAIN 562 570 POLY-GLY.
 FT DOMAIN 715 727 POLY-THR.
 FT DOMAIN 982 990 POLY-GLN.
 FT DOMAIN 1015 1049 POLY-ASN.
 FT DOMAIN 1598 1858 P13K/P14K.
 SQ SEQUENCE 1858 AA; 203945 MW; 228971F5 CRC32;

Query Match 9.9%; Score 852; DB 1; Length 1858;
 Best Local Similarity 35.5%; Pred. No. 3,24e-154;
 Matches 194; Conservative 122; Mismatches 179; Indels 52; Gaps 29;

DB 1339 RLKALMDS-DPLVQLSADKRLVGYRH-ITYSKPRALAKFL-LSVNMWIDPOVTDAYR 1395
 QY 577 KKLQMLVKKHESGIVLEEDQHRHVMWRRYIQOEPDLIVLSLAVWMDRENFSLTY 636
 DB 1396 QMNDMLKRVOLLEIDAFADENAVNFI-KTINSFSAESDFLOLTQVAKPEPH 1454
 QY 637 MLEKMPSPVAALVTLGKKTDRVIRKFAVEKINEQLSPVTHFLPLIOALKEPRA 696
 DB 1455 NSDLTHILORALSNSRIGHFFEMFLKSE--MHPEI--EE-RGILLGTYLSCGT 1507
 QY 697 QSEVGMMLLRALCD-YRIGHRLFMLRLAIARLROCDLSEERYRISLMEAYLKGNEE 755
 DB 1508 HRDDLKONOVLSLHTVANAVKQTNGSSRRKRYLMEGLSKIRFP-DTEPLPLDPWEAK 1566
 QY 756 HIRITROYDMVDELTRISTLVKGMKPDVATMK-LRDELNSISHKKNMNDSPIDPYKLG 814
 DB 1567 GLIIDCRVNSDKPLMLVFEVNEPRAK--PL-TVIEFVGGDLRODITLLOVLRIMDK 1622
 QY 815 EMITIDRAIVGSAKRPLMHMKKNKPSDLHLFCAMIFKNGDLDQDMLVQLVLEVMN 874
 DB 1623 FKNRSGMDRLQPYKCIATGIGMLEVNVNANTIANINKDAG--GTGALLEKTIYN-W 1679
 QY 875 IMKAANIDCOLNRYAVLPKEMIGIIEVVPNCKTIFEIOVGTFMNTAVRSDPSFMMRW 934
 DB 1680 L-KEC---N---KT--EA--E-YNKAVE-T-----F--I---L-SCAGYVATYMGIG 1714
 QY 935 IRKOCIEIEEKKSKKSDSTKNPIEKKIDNTQAMKFEESDRLYSCVGSVATYIMGK 994
 DB 1715 DRNSDMITKIGHLEHIDPGHGLGKYYKKGKREPARPITTPQYMAIV-6GK--D--S 1769
 QY 995 DRHSDMLLEDEKIVHDGHLGKTKLGIQRDRPFILTEHMTVIRSGKSDVGN 1054
 DB 1770 ENFRKRVTTCCSAYNILKRTDLEINLFOPLMSTGIPELOVADIDYLRKAL-APLSDE 1828
 QY 1055 HELQKFKTICVEAYEVMMNNRDLFVSLFTLMGLMELPELSTKADLDHLKTKLFCNGESEK 1114
 DB 1829 EAAEET 1835
 QY 1115 EAKKFEA 1121

RESULT 11
 ID P3K1 DICDI STANDARD; PRT: 1570 AA.
 AC P54673;
 DT 01-OCT-1996 (REL. 34, CREATED)

DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE PHOSPHATIDYLINOSITOL-3-KINASE 1 (EC 2.7.1.137) (P13-KINASE)
 DE (P13INS-3-KINASE) (P13K).
 GN P13A OR P13L.
 OS DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
 OC EUKARYOTA; DICTYOSTELIIDA; DICTYOSTELIUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AX3:
 RX MEDLINE; 96009592.
 RA ZHOU K., TAKEGAWA K., EMR S.D., FIRTLE R.A.;
 RT "A phosphatidylinositol (PI) kinase gene family in Dictyostelium
 RT discoidium: biological roles of putative mammalian p110 and yeast
 RT Vps34p PI 3-kinase homologs during growth and development.";
 RL MOL. CELL. BIOL. 15:5645-5656(1995).
 CC -1- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-ID-MYO-INOSITOL = ADP +
 CC -1- PHOSPHATIDYL-ID-MYO-INOSITOL-3-PHOSPHATE.
 CC -1- SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.
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DR EMBL: U23476; G733520; -
 DR DICTYDB: DD01099; P13A.
 DR PROSITE: PS00915; P13_4_KINASE_1; 1.
 DR PROSITE: PS00916; P13_4_KINASE_2; 1.
 DR PFAM: PF00454; P13_P14_KINASE; 1.
 DR PFAM: PF00613; P13Ka; 1.
 DR PFAM: PF00792; P13K_C2; 1.
 DR PFAM: PF00794; P13K_Ibd; 1.
 KW TRANSFERASE: KINASE; MULTIGENE FAMILY.
 FT DOMAIN 41 48 POLY-ASN.
 FT DOMAIN 59 73 POLY-ASN.
 FT DOMAIN 161 168 POLY-ASN.
 FT DOMAIN 284 304 POLY-THR.
 FT DOMAIN 308 324 POLY-THR.
 FT DOMAIN 413 424 POLY-ASN.
 FT DOMAIN 503 510 POLY-SER.
 FT DOMAIN 570 579 POLY-ASN.
 FT DOMAIN 821 828 POLY-ASN.
 FT DOMAIN 831 836 POLY-ASN.
 FT DOMAIN 1309 1570 P13K/P14K.
 SQ SEQUENCE 1570 AA; 178374 MW; B4A92817 CRC32;

Query Match 9.9%; Score 800; DB 1; Length 1570;
 Best Local Similarity 31.9%; Pred. No. 2,14e-142;
 Matches 213; Conservative 157; Mismatches 234; Indels 64; Gaps 37;

DB 965 IGWINVMTDFKYYLRQGVNELSLMPSDFSNPLGTCNNPSS-SQSVGLTLEEFENLPV 1023
 QY 479 VGMVNSLTDWMDLELRQGFLEHMAPEPTANRSRIGENGARIGNAVATIEISSYGRV 538
 DB 1024 LEPRKTKSTSVSVEIQ-PPT-NI-NSN-E--MR-FEQITAL--DPLSD--LKQERYN 1072
 QY 539 RMPGCGQYTYLVKHSRTETELNMGDDYESCIIRPGYKKLQMLVKKHESGIVLEEDQR 598
 DB 1073 QLMTLRHY-SILFPOVLRPLM-LSVPTQATAVDEAISLDRMPRLKRYSELELDAKHA 1130
 QY 599 HYMMWRRIYIQOEPDLIVLSLAVWMDRENFSLTYMLEKMPSPVAALVTLGKKTCT 658
 DB 1131 NKKVREAVTCL-EDLSDELDLILLOVQVLYKPEPFDKSLSRFLKALINRNIGHSF 1189
 QY 659 DRVIRKFAVEKINEQLSPVTHFLPLIOALKEPRAQSEVGMMLLRALCDVRIGHRL 718
 DB 1190 FMYLKSD---LHDSNL-SE---RGILLSELYIACGARIELLQMEYINNLTEVAKKIK 1242
 QY 719 FWLRLAETARLROCDLSEERYRISLMEAYLRNGNEHIKIRITROYDMVDELTRISTLVK 778

Db	Sequence	Score	Length	DB 1	DB 2	DB 3	DB 4	DB 5	DB 6	DB 7	DB 8	DB 9	DB 10	DB 11	DB 12	DB 13	DB 14	DB 15	DB 16	DB 17	DB 18	DB 19	DB 20	DB 21	DB 22	DB 23	DB 24	DB 25	DB 26	DB 27	DB 28	DB 29	DB 30	DB 31	DB 32	DB 33	DB 34	DB 35	DB 36	DB 37	DB 38	DB 39	DB 40	DB 41	DB 42	DB 43	DB 44	DB 45	DB 46	DB 47	DB 48	DB 49	DB 50	DB 51	DB 52	DB 53	DB 54	DB 55	DB 56	DB 57	DB 58	DB 59	DB 60	DB 61	DB 62	DB 63	DB 64	DB 65	DB 66	DB 67	DB 68	DB 69	DB 70	DB 71	DB 72	DB 73	DB 74	DB 75	DB 76	DB 77	DB 78	DB 79	DB 80	DB 81	DB 82	DB 83	DB 84	DB 85	DB 86	DB 87	DB 88	DB 89	DB 90	DB 91	DB 92	DB 93	DB 94	DB 95	DB 96	DB 97	DB 98	DB 99	DB 100	DB 101	DB 102	DB 103	DB 104	DB 105	DB 106	DB 107	DB 108	DB 109	DB 110	DB 111	DB 112	DB 113	DB 114	DB 115	DB 116	DB 117	DB 118	DB 119	DB 120	DB 121	DB 122	DB 123	DB 124	DB 125	DB 126	DB 127	DB 128	DB 129	DB 130	DB 131	DB 132	DB 133	DB 134	DB 135	DB 136	DB 137	DB 138	DB 139	DB 140	DB 141	DB 142	DB 143	DB 144	DB 145	DB 146	DB 147	DB 148	DB 149	DB 150	DB 151	DB 152	DB 153	DB 154	DB 155	DB 156	DB 157	DB 158	DB 159	DB 160	DB 161	DB 162	DB 163	DB 164	DB 165	DB 166	DB 167	DB 168	DB 169	DB 170	DB 171	DB 172	DB 173	DB 174	DB 175	DB 176	DB 177	DB 178	DB 179	DB 180	DB 181	DB 182	DB 183	DB 184	DB 185	DB 186	DB 187	DB 188	DB 189	DB 190	DB 191	DB 192	DB 193	DB 194	DB 195	DB 196	DB 197	DB 198	DB 199	DB 200	DB 201	DB 202	DB 203	DB 204	DB 205	DB 206	DB 207	DB 208	DB 209	DB 210	DB 211	DB 212	DB 213	DB 214	DB 215	DB 216	DB 217	DB 218	DB 219	DB 220	DB 221	DB 222	DB 223	DB 224	DB 225	DB 226	DB 227	DB 228	DB 229	DB 230	DB 231	DB 232	DB 233	DB 234	DB 235	DB 236	DB 237	DB 238	DB 239	DB 240	DB 241	DB 242	DB 243	DB 244	DB 245	DB 246	DB 247	DB 248	DB 249	DB 250	DB 251	DB 252	DB 253	DB 254	DB 255	DB 256	DB 257	DB 258	DB 259	DB 260	DB 261	DB 262	DB 263	DB 264	DB 265	DB 266	DB 267	DB 268	DB 269	DB 270	DB 271	DB 272	DB 273	DB 274	DB 275	DB 276	DB 277	DB 278	DB 279	DB 280	DB 281	DB 282	DB 283	DB 284	DB 285	DB 286	DB 287	DB 288	DB 289	DB 290	DB 291	DB 292	DB 293	DB 294	DB 295	DB 296	DB 297	DB 298	DB 299	DB 300	DB 301	DB 302	DB 303	DB 304	DB 305	DB 306	DB 307	DB 308	DB 309	DB 310	DB 311	DB 312	DB 313	DB 314	DB 315	DB 316	DB 317	DB 318	DB 319	DB 320	DB 321	DB 322	DB 323	DB 324	DB 325	DB 326	DB 327	DB 328	DB 329	DB 330	DB 331	DB 332	DB 333	DB 334	DB 335	DB 336	DB 337	DB 338	DB 339	DB 340	DB 341	DB 342	DB 343	DB 344	DB 345	DB 346	DB 347	DB 348	DB 349	DB 350	DB 351	DB 352	DB 353	DB 354	DB 355	DB 356	DB 357	DB 358	DB 359	DB 360	DB 361	DB 362	DB 363	DB 364	DB 365	DB 366	DB 367	DB 368	DB 369	DB 370	DB 371	DB 372	DB 373	DB 374	DB 375	DB 376	DB 377	DB 378	DB 379	DB 380	DB 381	DB 382	DB 383	DB 384	DB 385	DB 386	DB 387	DB 388	DB 389	DB 390	DB 391	DB 392	DB 393	DB 394	DB 395	DB 396	DB 397	DB 398	DB 399	DB 400	DB 401	DB 402	DB 403	DB 404	DB 405	DB 406	DB 407	DB 408	DB 409	DB 410	DB 411	DB 412	DB 413	DB 414	DB 415	DB 416	DB 417</
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QY 1062 TLCEVEYVMMNRDLVSLTLMGLMELBELSTKADLHLKTLFCNGESKEAKRFA 1121

DB 1459 KLHESI-GTATTINFAIHMAH 1481

QY 1122 GIYEAFNGSWSTKTMLEHAKH 1145

RESULT 13

ID VP34_SCHPO STANDARD: PRT: 801 AA.

AC P50520:

DT 01-OCT-1996 (REL. 34, CREATED)

DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE PHOSPHATIDYLINOSITOL 3-KINASE VP34 (EC 2.7.1.137) (PI3-KINASE)

DE (PTINS-3-KINASE) (PI3K) (VACUOLAR SORTING PROTEIN 34).

GN VP34.

OS SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

OC EUKARYOTA: FUNGI: ASCOMYCOTA: ARCHIASCOMYCETES:

OC SCHIZOSACCHAROMYCETALES: SCHIZOSACCHAROMYCETACEAE:

OC SCHIZOSACCHAROMYCETES.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE: 96360252.

RA TAKEGAWA K., DEMALD D.B., EMR S.E.:

RT "Schizosaccharomyces pombe Vps34p, a phosphatidylinositol-specific PI 3-kinase essential for normal cell growth and vacuole morphology."

RL CELL SCI. 108:3745-3756(1995).

CC 1- FUNCTION: PHOSPHATIDYLINOSITOL 3-KINASE HOMOLOG REQUIRED FOR VACUOLAR SORTING AND SEGREGATION.

CC 1- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-ID-MYO-INOSITOL - ADP + 1-PHOSPHATIDYL-ID-MYO-INOSITOL 3-PHOSPHATE.

CC 1- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.

CC

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CC

DR EMBL: U32583; G929997; -

DR PROSITE: PS00915; PI3_4_KINASE_1; 1.

DR PROSITE: PS00916; PI3_4_KINASE_2; 1.

DR PFAM: PF00454; PI3_P14_KINASE; 1.

DR PFAM: PF00613; PI3Ka; 1.

DR PFAM: PF00792; PI3K_C2; 1.

KW TRANSFERASE: KINASE.

FT DOMAIN 541 799

FT SEQUENCE 801 AA: 92135 MW: 1E514791 CRC32:

Query Match 5.38; Score 458; DB 1; Length 801;

Best Local Similarity 29.28; Pred. No. 1,42e-66;

Matches 167; Conservative 133; Mismatches 201; Indels 70; Gaps 44;

DB 282 LSEEDLWKRFRYTRKKAATKFLKSV--VWDSSEVNAALSLDSTETIDDALE 339

QY 592 LEEDEGRHVMNMKRYIQKEPDLIYLSELAFTWIRENSELYLVLEKWKPPSVAALTL 651

DB 340 LSPSPFVHKVAVAYASRL-ETASNEELLYLLOLQALRYNDPISDERFQSPIALTL 398

QY 652 LIGKRTDRAVIRKFAVEKLENDLSPYTFHLFIPLQALKE-P-----RAQ-SEVGMML 704

DB 399 VNRATSSPSIGNDLYWLYVEIE--D-EPVSKLFSSVVELFQKELSKVEGRILIRETL 454

QY 705 LTRALCDYRIGHRLFWLRLAETIARLDQDLKSEYRISILMAVYL-RGNEEH-IR-IIT 761

DB 455 AQAAPFKELIRTSKVSQSRGRFLKIEFLKLYLEHDKHLLDFAHLPDLPDSVNIIVGI 514

QY 762 RQVDWVDELTRISTLV---KGMF-KDYATMK-LRDELRSISHKEMENWSDPLDPVYKLGEM 816

DB 515 IPDACTVFTSQPLRLFLKFCQDG-SK-----Y-PIFFKNGDDLRQDQVLYQIQLTLMDKLL 568

QY 817 IIDKALVLSARPLMLHKKNNPKSDDLPLPCAMTFKNGDILRODMYLVLQYLEVMDNIM 876

DB 569 KKEKIDHLKPYRIATGPTHGAVQFVPS-KTLATI-L-AEY-HGSV--L-AVL-----R 616

QY 877 KANIDCCINPFAVLPNGMIGIEVVPNCKTIFELQVGTGMNTRAVRISIDSFNMKWR 936

DB 617 -E-NPDD---GL-NSA-N-YG--IDPV-AMDNV---V-R---SCAGCVITYLLGVDGR 658

QY 937 KQCGIDKKRSKSDSTKPNIEKIDNTQAMKKYFESVDPRFLYSCVGSVATYIMGIDKR 996

DB 659 HDNLILITKDGHEFHAEFGYITIGRD-PKL-F--S-PAMLSKE-M-V--EGWG-GYNSPF 708

QY 997 HSDNMLLTGDKVHIDFHEHILGHGKTKLGIORDROPFLTEHFMVIRSGSVDSGNSHE 1056

DB 709 YQOFKSCYTYTFALRKSNLILNLSLAVDANIPDIKDKKVVYKVERFCQMSSED 768

QY 1057 LQKFKLCYEAEEVMMNRNDLVSLTLMGLMELBELSTKADLHLKTLFCNGESKEE 1115

DB 769 AIKFEQLINDVSALFPQIIDRM-HNLAQY 798

QY 1116 ARKFEAGIYEAFNGSWSTKTMLEHAKH 1146

RESULT 14

ID P3K4_DICTDI STANDARD: PRT: 816 AA.

AC P54676;

DT 01-OCT-1996 (REL. 34, CREATED)

DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)

DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE PHOSPHATIDYLINOSITOL 3-KINASE VP34-LIKE (EC 2.7.1.137) (PI3-KINASE)

DE (PTINS-3-KINASE) (PI3K)

GN PIKE OR PIK5.

OS DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

OC EUKARYOTA: DICTYOSTELIIDA: DICTYOSTELIUM.

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN-AK3.

RX MEDLINE: 96009592.

RA ZHOU K., TAKEGAWA K., EMR S.D., FIRTLE R.A.:

RT "A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoidium: biological roles of putative mammalian p110 and yeast Vps34p PI 3-kinase homologs during growth and development."

RT MOL. CELL. BIOL. 15:5645-5656(1995).

CC 1- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-ID-MYO-INOSITOL - ADP + 1-PHOSPHATIDYL-ID-MYO-INOSITOL 3-PHOSPHATE.

CC 1- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.

CC

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CC

DR EMBL: U23480; G733530; -

DR DICTYDB: D001103; PIKE.

DR PROSITE: PS00915; PI3_4_KINASE_1; 1.

DR PROSITE: PS00916; PI3_4_KINASE_2; 1.

DR PFAM: PF00454; PI3_P14_KINASE; 1.

DR PFAM: PF00613; PI3Ka; 1.

DR PFAM: PF00792; PI3K_C2; 1.

KW TRANSFERASE: KINASE; MULTIGENE FAMILY.

FT DOMAIN 559 816

FT SEQUENCE 816 AA: 94647 MW: 25E09AF0 CRC32:

Query Match 4.58; Score 384; DB 1; Length 816;

Best Local Similarity 29.18; Pred. No. 6.58e-51;

Matches 151; Conservative 125; Mismatches 171; Indels 72; Gaps 48;

DB 309 IMRFRYLTNNKKAATKFLKSV--WSESHOKNKLSTIN-PKWDPIIDIASLSSAFT 365

QY 600 VMNMKRYIQKEPDLIYLSELAFTWTD-RENFSELYLVLEKWKPPSVAALTLIGKRC 658

GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 1999, 18:27:16 ; Search time 421.33 Seconds
(without alignments)
12686.225 Million cell updates/sec

Title: US-08-908-453-2

Sequence: 1 CGGAGCCCTGAGGCTCGAG.....ACGCACTCAACACTACTCA 3504

Scoring table: IDENTITY_NUC

Searched: 2002476 seqs, 762712212 residues

Database :

EST: *
1: em_est1: *
2: em_est2: *
3: em_est3: *
4: em_est4: *
5: em_est5: *
6: em_est6: *
7: em_est7: *
8: em_est8: *
9: em_est9: *
10: gp_est1: *
11: gp_est2: *
12: gp_est3: *
13: gp_est4: *
14: gp_est5: *
15: gp_est6: *
16: gp_est7: *
17: gp_est8: *
18: gp_est9: *
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38: gp_est19: *
39: gp_est20: *
40: gp_est21: *
41: gp_est22: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	374	10.7	374	22	C64227 C.elegans C
2	360	10.3	360	22	C61935 C.elegans C

RESULT	LOCUS	DEFINITION	ACCESSION	NID	KEYWORDS	SOURCE	ORGANISM	TITLE	JOURNAL	REFERENCE	AUTHORS
1	C64227	C.elegans CDNA clone yk355b7 : 5' end, single read, mRNA sequence.	C64227	92422932	EST: EST(expressed sequence tag).	Caenorhabditis elegans (Strain: CB1489 hlm-8(e1489)) varied hermaphrodite, male whole animal CDNA to mRNA, clone_1lb.yuj1 Kohara unpublished CDNA library clone: yk355b7.	Caenorhabditis elegans	Submitted (23-Jul-1997) to the DBJ/EMBL/GenBank databases. Yuj1 Kohara, National Institute of Genetics, Gene Network Lab, Yatai III, Mishima, Shizuoka 411, Japan (E-mail: ykohara@lab.nig.ac.jp).			

ALIGNMENTS

3	347	9	9	360	22	C60236	C60236 C.elegans C
4	281	8.0	360	22	C68381	C68381 C.elegans C	
5	215	6.1	240	19	C12541	C12541 C.elegans C	
6	200.8	5.7	240	22	C65154	C65154 C.elegans C	
7	174	5.0	300	22	C51288	C51288 C.elegans C	
8	168.4	4.8	300	19	C10729	C10729 C.elegans C	
9	166	4.7	300	22	C54056	C54056 C.elegans C	
10	149.4	4.3	300	22	C52578	C52578 C.elegans C	
11	135.8	3.9	300	22	C54778	C54778 C.elegans C	
12	132	3.8	329	10	M79683	M79683 WES00220 C	
13	91.2	2.6	447	39	A155136	A155136 uds9f06.r	
14	74.2	2.1	231	22	C57311	C57311 C.elegans C	
15	73.4	2.1	476	16	AA174738	AA174738 mt12e11.r	
16	72	2.1	328	10	R12466	R12466 y136n07.tl	
17	65.6	1.9	367	16	AA124657	AA124657 mq72c02.r	
18	64.8	1.8	324	11	T29663	T29663 EST89481 Ho	
19	64	1.8	437	20	AA542224	AA542224 vk28a04.r	
20	63.2	1.8	667	36	AA206574	AA206574 zq51g02.r	
21	61.8	1.8	392	41	A1166295	A1166295 xylem.est	
22	60.2	1.7	509	10	R21085	R21085 y952f07.tl	
23	60.2	1.7	330	10	R22699	R22699 y908e01.tl	
24	60	1.7	360	20	CEK1054AF	D75478 C.elegans C	
25	59.6	1.7	263	10	R18590	R18590 yf96b10.tl	
26	55.4	1.6	331	20	AA445047	AA445047 yq57h11.r	
27	55	1.6	391	15	AA190747	AA190747 zp88d05.r	
28	52.6	1.5	533	41	A1162454	A1162454 A01/P690	
29	49.6	1.4	362	37	C82811	C82811 Oryctolagus	
30	49.6	1.4	362	37	C83667	C83667 Oryctolagus	
31	48.6	1.4	357	22	AA571816	AA571816 V191f09.r	
32	48	1.4	574	34	AB009107	AB009107 Chlamydom	
33	46.6	1.3	750	39	A1158022	A1158022 uds2a08.r	
34	46	1.3	475	19	AA437822	AA437822 ve3q12.r	
35	45.6	1.3	386	37	C94469	C94469 Dictyostel	
36	45	1.3	433	14	W76227	W76227 z664c12.tl	
37	45	1.3	396	22	AA229699	AA229699 nc37g11.s	
38	44.2	1.3	336	11	T31157	T31157 EST28078 Ho	
39	44.2	1.3	292	20	HMW420G03B	D56232 Human fetal	
40	43	1.2	357	38	RICR1770A	D24330 Rice CDNA	
41	41.2	1.2	274	17	AA298224	AA298224 EST113806	
42	40.8	1.2	413	36	AA861836	AA861836 ak39a08.s	
43	40.4	1.2	403	33	AA424309	AA424309 zv90c11.r	
44	39.4	1.1	375	19	C12533	C12533 C.elegans C	
45	39	1.1	441	40	A1231484	A1231484 EST228172	

1111, Mishima, Shizuoka 411, Japan (E-mail: ykohara@lab.nig.ac.jp)

/organism="Caenorhabditis elegans"

/strain="CB1489 him-8(el489)"
 /db_xref="taxon:6239"
 /clone="YK192d4"
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 /dev_stage="varied"
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 /tissue_type="whole animal"
 /lssue_type="whole animal"

BASE COUNT 112 a 65 c 82 g 100 t 1 others

ORIGIN

Query Match 9.9%; Score 347; DB 22; Length 360;
 Best Local Similarity 99.4%; Pred. No. 2.5e-84;

Matches 358; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1240 CTTATGATGAGGCGCTGTG-AATATTTCTGATTCGATTTCCCGCGAGCTGATATGTA 1298
 DB 1 CTTATGAGGCGCTGTGAAATTTCTGATTCGATTTCCCGCGAGCTGATATGTA 60
 QY 1299 CGTTGCAATGCAATTCAGTATATGTTGGGACATGACGCTGGCATCAAAATCTACAC 1358
 DB 61 CGTTGCAATGCAATTCAGTATATGTTGGGACATGACGCTGGCATCAAAATCTACAC 120
 QY 1359 AAAAGCATGCTCATTTGCAAAAATGAAATAGAAATGATACATTGATCTATACAT 1418
 DB 121 AAAAGCATGCTCATTTGCAAAAATGAAATAGAAATGATACATTGATCTATACAT 180
 QY 1419 GAAGATATGCGCATCTGACATCTGACATCTGCTGTTTGTAGGAAAATGAAAT 1478
 DB 181 GAAGATATGCGCATCTGACATCTGACATCTGCTGTTTGTAGGAAAATGAAAT 240
 QY 1479 AAAAGTGAAGATTTGAAAGTTGGTGAATATGTCCTTAACGATTTGAGAGATGA 1538
 DB 241 AAAAGTGAAGATTTGAAAGTTGGTGAATATGTCCTTAACGATTTGAGAGATGA 300
 QY 1539 ACTACGACAGGACATTTTATTCATCTGTGGCTCCGAAACGACATCCCATCTAG 1598
 DB 301 ACTACGACAGGACATTTTATTCATCTGTGGCTCCGAAACGACATCCCATCTAG 360

RESULT 4

LOCUS C68381 360 bp mRNA EST 29-AUG-1997
 DEFINITION C.elegans cDNA clone yk302a12 : 5' end, single read, mRNA sequence.
 ACCESSION C68381
 NID 92429737
 KEYWORDS EST: EST(expressed sequence tag).
 SOURCE Caenorhabditis elegans (strain:CB1489 him-8(el489)) varied hermaphrodite, male whole animal cDNA to mRNA, clone_lib:Yuji Kohara unpublished cDNA library clone:yk302a12.

ORGANISM

Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae; Rhabditina; Rhabditidae; Rhabditidae; Pelodierinae; Caenorhabditis. 1 (sites)
 Kohara, Y., Motohashi, T., Tabara, H., Shin-i, T., Watanabe, H., Sano, M., Miyata, A., Ohba, T., Mitani, Y., Uesugi, H., Sugiyama, I., Ohara, M., Sugimoto, A., Iida, K. and Nishigaki, A.

TITLE Expression map of the C.elegans genome
 JOURNAL Unpublished (1997)
 REFERENCE 2 (bases 1 to 360)
 AUTHORS Kohara, Y.
 JOURNAL Direct Submission
 TITLE Submitted (23-JUL-1997) to the DDBJ/EMBL/GenBank databases. Yuji Kohara, National Institute of Genetics, Gene Network Lab; Yata 1111, Mishima, Shizuoka 411, Japan (E-mail:ykohara@lab.nig.ac.jp, Tel:+81-559-81-6854, Fax:+81-559-81-6855)

FEATURES

source
 1. 360
 /organism="Caenorhabditis elegans"
 /strain="CB1489 him-8(el489)"
 /db_xref="taxon:6239"
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 /clone_lib="Yuji Kohara unpublished cDNA library"

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 /tissue_type="whole animal"
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BASE COUNT 115 a 68 c 77 g 99 t 1 others

ORIGIN

Query Match 8.0%; Score 281; DB 22; Length 360;
 Best Local Similarity 99.0%; Pred. No. 2.6e-66;
 Matches 303; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 3201 GGGTAATCTGTGATG-AAAATTCGATGACCTACAAAATTCAAAACGATATGCTG 3259
 DB 1 GGGTAATCTGTGATGAAAATTCGATGACCTACAAAATTCAAAACGATATGCTG 60
 QY 3260 AAGCCACG-AAGTATGGAATATGAGATTTGCTTCTGTTGACCTGATG 3318
 DB 61 AAGCCACGAAATATGGAATATGAGATTTGCTTCTGTTGACCTGATG 120
 QY 3319 CTCGGAATGAGTTGCTGAGCTGTCGACGAAAGCGATTTGATCATTTGAAGAAACC 3378
 DB 121 CTCGGAATGAGTTGCTGAGCTGTCGACGAAAGCGATTTGATCATTTGAAGAAACC 180
 QY 3379 CTCCTGCAATGAGCAAAAGCAAGAGAGAGAAATTTTGGCTGGAATCTACGA 3438
 DB 181 CTCCTGCAATGAGCAAAAGCAAGAGAGAGAAATTTTGGCTGGAATCTACGA 240
 QY 3439 GAAGCTTCATGATGATGATGCTGCTACCAAGAAATGCTTCACGACGTCACAAAC 3498
 DB 241 GAAGCTTCATGATGATGCTGCTACCAAGAAATGCTTCACGACGTCACAAAC 300
 QY 3499 TACTGA 3504
 DB 301 TACTGA 306

RESULT 5

LOCUS C12541 240 bp mRNA EST 09-SEP-1996
 DEFINITION C.elegans cDNA clone yk152c9 : 5' end, single read, mRNA sequence.
 ACCESSION C12541
 NID 91560094
 KEYWORDS EST: EST(expressed sequence tag).
 SOURCE Caenorhabditis elegans (strain:CB1489 him-8(el489)) varied male whole animal cDNA to mRNA, clone_lib:Yuji Kohara unpublished cDNA clone:yk152c9.

ORGANISM

Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae; Rhabditina; Rhabditidae; Pelodierinae; Caenorhabditis. 1 (sites)
 Kohara, Y., Motohashi, T., Tabara, H., Watanabe, H., Sugimoto, A., Sano, M., Miyata, A. and Nishigaki, A.

TITLE Expression map of the C.elegans genome
 JOURNAL Unpublished (1996)
 REFERENCE 2 (bases 1 to 240)
 AUTHORS Kohara, Y.
 JOURNAL Direct Submission
 TITLE Submitted (29-APR-1996) to the DDBJ/EMBL/GenBank databases. Yuji Kohara, National Institute of Genetics, Gene Network Lab; Yata 1111, Mishima, Shizuoka 411, Japan (E-mail:ykohara@lab.nig.ac.jp, Tel:0559-81-6854, Fax:0559-81-6855)

FEATURES

source
 1. 240
 /organism="Caenorhabditis elegans"
 /strain="CB1489 him-8(el489)"
 /db_xref="taxon:6239"
 /clone="YK152c9"
 /clone_lib="Yuji Kohara unpublished cDNA"
 /dev_stage="varied"
 /sex="male"
 /tissue_type="whole animal"

BASE COUNT 74 a 42 c 59 g 61 t 4 others

REFERENCE	TITLE	AUTHORS	ORGANISM	KEYWORDS	SOURCE
ACCSSION NID C10729					
EST: EST(expressed sequence tag)					
Caenorhabditis elegans (strain:CB1489 him-8(e1489)) varied male					
whole animal cDNA to mRNA, clone_1lb:Yuj1 Kohara unpublished cDNA					
clone:YK152c9.					
Caenorhabditis elegans					
Eukaryotes; mitochondrial eukaryotes; Metazoa; Nematoda;					
Secernentea; Rhabditia; Rhabditidae; Rhabditidae; Rhabditidae;					
Rhabditidae; Peloderinae; Caenorhabditis.					
1 (sites)					
Kohara, Y., Mochizuki, T., Tabara, H., Watanabe, H., Sugimoto, A.,					
Sano, M., Miyata, A. and Nishigaki, A.					
Expression map of the C.elegans genome					
Unpublished (1996)					
2 (bases 1 to 300)					
Kohara, Y.					
Direct Submission					
Submitted (29-APR-1996) to the DDBJ/EMBL/GenBank databases. Yuj1					
Kohara, National Institute of Genetics, Gene Library Lab. Yata					
111, Mishima, Shizuoka 411, Japan (E-mail: ykohara@elab.nig.ac.jp,					
Tel:0559-81-6854, Fax:0559-81-6855)					
Location/Qualifiers					
1..300					
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/clone="YK152c9"					
/clone_1lb="Yuj1 Kohara unpublished cDNA"					
/dev_stage="varied"					
/sex="male"					
/tissue_type="whole animal"					
/base_count 89 a 49 c 76 g 84 t 2 others					
BASE COUNT					
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Best Local Similarity	98.8%	Prod. No. 1.4e-35			
Matches 169	Conservative	0	Mismatches 3	Indels 0	Gaps 0
Y 3334	CCTGAGCTGTGACGAAAGCGATTGGATCATCTTTGAAGAAACCTCTTCGATGGA	3393			
Db 300	CCTGAGCTGTGACGAAAGCGATTGGATCATCTTTGAAGAAACCTCTTCGATGGA	241			
Y 3394	GAAAGCAAGAAAGAGCGAAGAAAGTTTTCGCTGGAATCTACGAAGAACCTTCATGGA	3453			
Db 240	GAAAGCAAGAAAGAGCGAAGAAAGTTTTCGCTGGAATCTACGAAGAACCTTCATGGA	181			
Y 3454	TCATGCTTACCAAAACGATTTGGCTCTTCACGACGATCAACACTACTGGA	3504			
Db 180	TCATGCTTACCAAAACGATTTGGCTCTTCACGACGATCAACACTACTGGA	130			
RESULT 9					
LOCUS	CS4056	300 bp	mRNA	EST	29-AUG-1997
DEFINITION	C.elegans cDNA clone YK155b7 : 3' end, single read, mRNA sequence.				
ACCSSION	CS4056				
NID	92391813				
KEYWORDS	EST: EST(expressed sequence tag)				
SOURCE	Caenorhabditis elegans (strain:CB1489 him-8(e1489)) varied male				
ORGANISM	Caenorhabditis elegans				
REFERENCE	Eukaryotes; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;				
AUTHORS	Rhabditidae; Peloderinae; Caenorhabditis.				
TITLE	1 (sites)				
AUTHORS	Kohara, Y., Mochizuki, T., Tabara, H., Shin, I.-T., Watanabe, H.,				
JOURNAL	Sano, M., Miyata, A., Ohta, T., Mitani, Y., Uesugi, H., Sugitani, I.,				
REFERENCE	Obara, M., Sugimoto, A., Iida, K. and Nishigaki, A.				
UNPUBLISHED	Expression map of the C.elegans genome				
REFERENCE	Unpublished (1997)				
2 (bases 1 to 300)					

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BASE COUNT	91 a 49 c 73 g 86 t 1 others
ORIGIN	
Query Match	4.7%; Score 166; DB 22; Length 300;
Best Local Similarity	100.0%; Pred. No. 6.3e-35;
Matches 166; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY 3339	GCTGCGACGAAGCGGATTTGCATCATTTGAAGAAACCCCTTCGTCAGTGAAGAAG 3398
DB 300	GCTGTCGACGAAGGCGGATTTGGATCATTTGAAGAAACCCCTTCGTCAGTGAAGAAG 241
QY 3399	CAAGAAGAGCGAAGAGTTTTCGCTGCGATCTACGACAGAGAGCCCTCAATGATCATG 3458
DB 240	CAAGAAGAGCGAAGAGTTTTCGCTGCGATCTACGACAGAGAGCCCTCAATGATCATG 181
QY 3459	GCTCTACCAAAAGCATTTGGCTCTTCACAGCAGTCAAAACACTACTGA 3504
DB 180	GCTCTACCAAAAGCATTTGGCTCTTCACAGCAGTCAAAACACTACTGA 135

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RESULT 10
C52578/c
LOCUS C52578 300 bp mRNA EST 29-AUG-1997
DEFINITION C.elegans cDNA clone yk260g10 : 3' end, single read, mRNA sequence.
ACCESSION C52578
NID 92390335
KEYWORDS EST; EST(expressed sequence tag).
SOURCE Caenorhabditis elegans (strain:CB1489 him-8(el489)) varied
hemaphrodite, male whole animal cDNA to mRNA, clone_lib:yuj1
Caenorhabditis elegans
Caenorhabditis elegans
Euarvotae; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidae; Rhabditidae; Pelodertinae; Caenorhabditis.
1 (sites)
kohara.Y., Motobashiri.T., Tabara.H., Shih-I.T., Watanabe.H.,
Sano.M., Miyata.A., Ohda.T., Mitani.Y., Uesugi.H., Sugitani.I.,
Obara.M., Sugimoto.A., Iida.K. and Nishigaki.A.
Expression map of the C.elegans genome
Unpublished (1997)
2. (bases 1 to 300)
kohara.Y.
Direct Submission
Submitted (23-JUL-1997) to the DDBJ/EMBL/Genbank databases. yuj1
kohara, National Institute of Genetics, Gene Network Lab, Yata
1111, Mishima, Shizuoka 411, Japan (E-mail: yk@kohara@lab.nig.ac.jp,
Tel:+81-559-81-6854, Fax:+81-559-81-6855)
FEATURES
Source
location/qualifiers
1..300
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(el489)"
/db_xref="taxon:6239"
/clone="yk260g10"
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BASE COUNT 93 a 46 c 69 g 87 t 5 others
ORIGIN

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Best Local Similarity 98.0%; Pred. No. 2.1e-30;
Matches 150; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3352 GCGGATTGGATCATTTGAAGAAACCCTCTTGTGCAATGAGAGAAAGCAAGAGCG 3411
|||||
Db 300 GCGGATTGGATCATTTGAAGAAACCCTCTTGTGCAATGAGAGAGCAAGAGCG 241

OY 3412 AGAAGTTTTCGTCGATCTACGAAGAACCTTCATGATGATGCTTACCAAAAGC 3471
|||||
Db 240 AGAAGTTTTCGTCGATCTACGAAGAACCTTCATGATGATGCTTACCAAAAGC 181

OY 3472 AATTGGCTCTTCACGAGTCGCAAACTACTGA 3504
|||||
Db 180 AATTGGCTCTTCACGAGTCGCAAACTACTGA 148

RESULT 11
LOCUS C54778 300 bp mRNA EST 29-AUG-1997
C54778/c
DEFINITION C.elegans cDNA clone yk360d11 : 3' end, single read, mRNA sequence.
ACCESSION C54778
NID 92399379
KEYWORDS EST; EST(expressed sequence tag).
SOURCE Caenorhabditis elegans (strain:CB1489 him-8(e1489)) varied hermaphrodite, male whole animal cDNA to mRNA, clone_11b:yuj1
ORGANISM Kohara unpublished cDNA library clone:yk360d11.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditiida; Rhabditida; Rhabditina; Rhabditidae; Pelodderinae; Caenorhabditis.

REFERENCE 1 (sites)
AUTHORS Kohara, Y., Morohashi, T., Tabara, H., Shin-I, T., Matanabe, H., Sano, M., Miyata, A., Ohba, T., Mitani, Y., Desugli, H., Sugita, I., Obara, M., Sugimoto, A., Iida, K. and Nishigaki, A.
TITLE Expression map of the C.elegans genome
JOURNAL Unpublished (1997)
REFERENCE 2 (bases 1 to 300)
AUTHORS Kohara, Y.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1997) to the DDBJ/EMBL/Genbank databases. Yuj1 Kohara, National Institute of Genetics, Gene Network Lab; Yata 1111, Mishima, Shizuoka 411, Japan (E-mail:ykohara@lab.nig.ac.jp, Tel:+81-559-81-6854, Fax:+81-559-81-6855)

FEATURES
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/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
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/sex="hermaphrodite, male"
/tissue_type="whole animal"
BASE COUNT 94 a 47 c 56 g 92 t 11 others
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Best Local Similarity 93.3%; Pred. No. 1.1e-26;
Matches 140; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3355 GATTGGATCATTTGAAGAAACCCTCTTGTGCAATGAGAGAAAGCAAGAGCGAGA 3414
|||||
Db 300 GATTGGATCATTTGAAGAAACCCTCTTGTGCAATGAGAGAAAGCAAGAGCGAGA 241

OY 3415 AAGTTTTCGTCGATCTACGAAGAACCTTCATGATGATGCTTACCAAAAGAT 3474
|||||
Db 240 AAGTTTTCGTCGATCTACGAAGAACCTTCATGATGATGCTTACCAAAAGAT 181

OY 3475 TGGCTCTTCACGAGTCGCAAACTACTGA 3504
|||||
Db 180 TGGCTCTTCACGAGTCGCAAACTACTGA 151

RESULT 12
LOCUS M79683 329 bp mRNA EST 30-JUN-1992
M79683/c
DEFINITION WEST00220 Caenorhabditis elegans cDNA clone CEMSC28.
ACCESSION M79683
NID 9271704
KEYWORDS EST
SOURCE Nematodes clone-CEMSC28 library-Mixed stage, Striatagene (cat. #937006) vector-Uni-ZAP XR primer-M13 Foward C. elegans mixed stage cDNA library. Striatagene catalog #937006. The library is oligo dT primed and directionally cloned in the Uni-ZAP XR vector.
ORGANISM Caenorhabditis elegans
Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditiida; Rhabditina; Rhabditidae; Pelodderinae; Caenorhabditis.

REFERENCE 1 (bases 1 to 329)
AUTHORS McCombie, W.R., Adams, M.D., Kelley, J.M., Fitzgerald, M.G., Fields, C., Utterback, T.R., Khan, M., Dubnick, M., Kerlavage, A.R., Venter, J. and
TITLE Caenorhabditis elegans expressed sequence tags reveal gene families and potential disease gene homologues
JOURNAL Nature Genet. 1, 124-131 (1992)
COMMENT Contact: Kerlavage AR
The Institute for Genomic Research
932 Clopper Road, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: arkerlavage@igf.org.

FEATURES
source
1..329
/organism="Caenorhabditis elegans"
/clone="CEMSC28"
BASE COUNT 110 a 46 c 72 g 97 t 4 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.3e-25;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

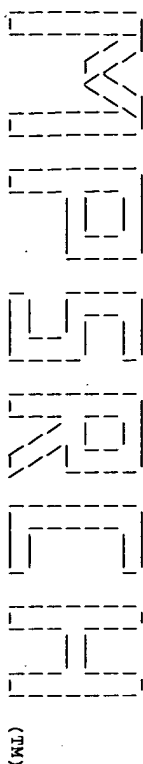
OY 3373 AAAACCCCTTTCGCAATGAGAGAAAGCAAGAGCGAGAAAGTTCCTCGATC 3432
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Db 329 AAAACCCCTTTCGCAATGAGAGAGCAAGAGCGAGAAAGTTCCTCGATC 270

OY 3433 TAGAAGAGCCCTTCATGATGATGCTTACCAAAAGATGGCTCTCCAGCAGTC 3492
|||||
Db 269 TAGAAGAGCCCTTCATGATGATGCTTACCAAAAGATGGCTCTCCAGCAGTC 210

OY 3493 AAACACTACTGA 3504
|||||
Db 209 AAACACTACTGA 198

RESULT 13
LOCUS A1155136 447 bp mRNA EST 30-SEP-1998
A1155136
DEFINITION uds9f06.r1 Soares mouse uterus NMPu Mus musculus cDNA clone 1450211
5' similar to SW-PL1A.MOUSE P42337 PHOSPHATIDYLINOSITOL 3-KINASE
CATALYTIC SUBUNIT, ALPHA ISOFORM ;, mRNA sequence.
ACCESSION A1155136
NID 93683605
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 447)
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and



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Msrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Jul 16 17:09:58 1999; Maspar time 46.23 Seconds
527.154 Million cell updates/sec
Tabular output not generated.

Title: >US-08-908-453-1
Description: (1-1146) from US08908453.pep
Perfect Score: 8617
Sequence: 1 MHVNIHPOLQTVWEQWQMR.....AFNGSMTKTNWLFHAKVHY 1146

Scoring table: PAM 150
Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 39.883; Variance 187.451; scale 0.213

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	8617	100.0	1146	31	W47544	Ceenorhabditis elegans	0.00e+00
2	1166	13.5	1068	9	R46294	Pcdins 3-Kinase 110 k	1.97e-89
3	1151	13.4	1068	9	R43341	p110.	4.35e-88
4	1151	13.4	1068	8	R43342	Human p110.	4.35e-88
5	981	11.4	1102	39	W90083	Porcine G-protein reg	6.76e-73
6	981	11.4	1102	31	W23948	Porcine phosphoinosit	6.76e-73
7	962	11.2	1044	33	W58570	Human phosphatidylin	3.33e-71
8	961	11.2	1101	39	W90089	Human G-protein regul	4.09e-71
9	960	11.1	1044	29	W46625	Mammalian novel class	5.01e-71
10	937	10.9	1101	31	W23947	Human phosphoinositid	5.59e-69
11	925	10.7	1050	20	W11576	Human phosphatidylin	6.52e-68
12	925	10.7	1050	20	W11577	Human phosphatidylin	6.52e-68
13	599	7.0	1726	29	W38756	Phosphatidyl inositol	3.42e-39
14	590	6.8	1686	34	W70991	Human class II PI3 Ki	2.08e-38
15	436	5.1	1876	29	W38757	Phosphatidyl inositol	3.75e-25
16	216	2.3	817	27	W37498	Human NP1K.	4.55e-07

17	216	2.5	829	27	W37499	Human NP1K.	4.55e-07
18	137	2.3	127	9	R45552	Human P1TR-C.	1.32e-05
19	200	2.3	131	9	R45553	Human P1TR-F.	7.81e-06
20	155	1.8	1140	16	R81731	GST-SEP fusion protei	1.77e-02
21	155	1.8	2549	19	W04235	Human RAP1.	1.77e-02
22	155	1.8	2549	16	R81730	Strolium effector pr	1.77e-02
23	155	1.8	2549	32	W56027	FRAP (cor1) protein.	1.77e-02
24	151	1.8	3055	32	W19693	ATM mutant 8578del3.	3.43e-02
25	150	1.6	562	19	W04236	Candida RAP1-like pr	2.07e-01
26	140	1.6	2932	22	W19675	ATM mutant 2467del372	2.07e-01
27	140	1.6	2989	22	W19688	ATM mutant 1407del1201	2.07e-01
28	140	1.6	2989	22	W19691	ATM mutant 3403del1174	2.07e-01
29	140	1.6	2998	22	W19673	ATM mutant 3403del1174	2.07e-01
30	140	1.6	3001	22	W19692	ATM mutant 4612del1155	2.07e-01
31	140	1.6	3003	22	W19670	ATM mutant 4612del1155	2.07e-01
32	140	1.6	3003	22	W19658	ATM mutant 7630del1159	2.07e-01
33	140	1.6	3005	22	W19648	ATM mutant 9001del105	2.07e-01
34	140	1.6	3021	22	W19661	ATM mutant 6348del1105	2.07e-01
35	140	1.6	3026	22	W19676	ATM mutant 2377del190.	2.07e-01
36	140	1.6	3046	22	W19690	ATM mutant C9140T.	2.07e-01
37	140	1.6	3054	22	W19695	ATM mutant 7279del16.	2.07e-01
38	140	1.6	3054	22	W19702	ATM mutant 5435del11.	2.07e-01
39	140	1.6	3055	22	W19697	ATM mutant 7278del16.	2.07e-01
40	140	1.6	3056	32	W37133	Ataxia-relanglectasia	2.07e-01
41	140	1.6	3056	27	W07653	Ataxia-relanglectasia	2.07e-01
42	140	1.6	3056	27	W19699	ATM mutant Leu43Pro.	2.07e-01
43	140	1.6	3056	27	W06234	ATM protein.	2.07e-01
44	140	1.6	3059	22	W19696	ATM mutant 5319ins9.	2.07e-01
45	140	1.6	3085	22	W19701	ATM mutant G9170C.	2.07e-01

ALIGNMENTS

RESULT 1
ID W47544 standard; Protein: 1146 AA.

AC W47544.
DE 03-AUG-1998 (first entry)

DR Ceenorhabditis elegans AGE-1 polypeptide.
DT age-1 gene; AGE-1 polypeptide; longevity; increase; onset; delay;
KW age-related conditions; pesticides; insects; nematodes; detection;
KW PI3K; phosphatidylinositol-3-kinase.

OS Ceenorhabditis elegans.

FN Key Location/Qualifiers
FT Region 852..864
FT /note="Conserved region"

FT Region 1111..1116
FT /note="Conserved region"

PN W09805761-AL.
PD 12-FEB-1998.
PF 07-AUG-1997; U13914.

PR 07-AUG-1996; US-023382.
PA (GENE) GEN HOSPITAL CORP.

PI Morris J. Ruvkun G. Tissenbaum H;
DR WPI: 98-145603/13.
DR N-PEDB: V18654.

PT AGE-1 polypeptide(s) and related nucleic acid, vectors, transformed
PT cells - and antibodies, used to determine longevity of animals and
PT to identify modulators, potentially useful for increasing longevity

PS Claim 1: Fig 6: 54pp: English.

The sequence is that of the AGE-1 polypeptide. AGE-1 is a
phosphatidylinositol-3-kinase (PI3K) involved in control
of senescence. Reduced AGE-1 mediated signalling increases longevity
while complete abrogation causes developmental arrest. Agents
that decrease expression or activity are used to increase
longevity (delay the onset of age-related conditions) in a mammal.

They can be used as pesticides (against insects and nematodes).
Since the agents target invertebrate diapause events, they are
safer pesticides than compounds that inhibit neuro-transmission.

Measurement of age-1 gene expression or AGE-1 protein activity can
be used in the determination of the longevity of an animal.

Sequence 1146 AA.

Query Match 100.0%; Score 8617; DB 31; Length 1146;

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Best Local Similarity 100.0%; Pred.No. 0.00e+00;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	1	mhvnlhpbqqtmevqgmreerpslstenogksllleneqvadlltmrpfseivslsvpw	60
Dh	61	flavnrtslelksldsfkfhqfjelljapmkwctysvkpqdyvfrqnlmfeleivfnddqp1	120
Qy	61	flavnrtslelksldsfkfhqfjelljapmkwctysvkpqdyvfrqnlmfeleivfnddqp1	120
Dh	121	sklshlbtcfmflilyvpdginrdkmlmsdshncjysldklsesideelrqfiraslwart	180
Qy	121	sklshlbtcfmflilyvpdginrdkmlmsdshncjysldklsesideelrqfiraslwart	180
Dh	181	ktctltgltgtsiyafpreeqytlcvgesopkdaesvvkaaklsysgmfwrkkaelngnce	240
Qy	181	ktctltgltgtsiyafpreeqytlcvgesopkdaesvvkaaklsysgmfwrkkaelngnce	240
Dh	241	kmmkltqiefnpuepkx1lhtflyemrkldvydtdddadegwflqlagrtcfvtpndk1	300
Qy	241	kmmkltqiefnpuepkx1lhtflyemrkldvydtdddadegwflqlagrtcfvtpndk1	300
Dh	301	tsydgvrselesyrcpbfvvrqsgllykcyctrpkrplyephvyrahertaladvsids	360
Qy	301	tsydgvrselesyrcpbfvvrqsgllykcyctrpkrplyephvyrahertaladvsids	360
Dh	361	tpkpskshdmmdfrptaslkvswlddanlmtprvylsgfdfrpadmdmvrtefevy	420
Qy	361	tpkpskshdmmdfrptaslkvswlddanlmtprvylsgfdfrpadmdmvrtefevy	420
Dh	421	vglctlasakctkyvaqfakwnkemytfdllymkdmpsaavlslrlylykvklkseefevg	480
Qy	421	vglctlasakctkyvaqfakwnkemytfdllymkdmpsaavlslrlylykvklkseefevg	480
Dh	481	wymmsltdwrdelirggqflhlwapeptanrsrfigengarjstnaavtelssyvgvrtm	540
Qy	481	wymmsltdwrdelirggqflhlwapeptanrsrfigengarjstnaavtelssyvgvrtm	540
Dh	541	psggqgytvllykhsrtwecelnmgddyescirpdykklqmlvykkesgylveedegrhv	600
Qy	541	psggqgytvllykhsrtwecelnmgddyescirpdykklqmlvykkesgylveedegrhv	600
Dh	601	wmmrry1qkgepdlllylajelafwtdrenfiselylmlekwkpsvaaal1llykrtcdr	660
Qy	601	wmmrry1qkgepdlllylajelafwtdrenfiselylmlekwkpsvaaal1llykrtcdr	660
Dh	661	vtrfaveklineqspvtfnllflrlp1lqalkyprgrqsevgmml1tralcdrjghrtfw	720
Qy	661	vtrfaveklineqspvtfnllflrlp1lqalkyprgrqsevgmml1tralcdrjghrtfw	720
Dh	721	llreleirldcdlkseeyrrisllmeaylyrgneelklltrqvdmdveltristclygm	780
Qy	721	llreleirldcdlkseeyrrisllmeaylyrgneelklltrqvdmdveltristclygm	780
Dh	781	pkdvaemkldelirslshkmemndsp1dpyvklgemldkcalvlgaskrplmlhknknp	840
Qy	781	pkdvaemkldelirslshkmemndsp1dpyvklgemldkcalvlgaskrplmlhknknp	840
Dh	841	ksdthlpfcmalfnngddlvcqdmlylqvlyewmdhlykaanldccclnpyavlypmgemlgl	900
Qy	841	ksdthlpfcmalfnngddlvcqdmlylqvlyewmdhlykaanldccclnpyavlypmgemlgl	900
Dh	901	evybncktlfeiqvgtgfmntlavrsldpsfmbkwilrkqsgidekkkskdgstnrlp1jkk	960
Qy	901	evybncktlfeiqvgtgfmntlavrsldpsfmbkwilrkqsgidekkkskdgstnrlp1jkk	960
Dh	961	idntqamkkyfsevdrllyscvgsyvaetylmglkdisdnalm1tedqkvvhldfghllgh	1020
Qy	961	idntqamkkyfsevdrllyscvgsyvaetylmglkdisdnalm1tedqkvvhldfghllgh	1020
Dh	1021	gktklgldqrdflltenhmtvlyrsgksvqdnshelqfktclcvaeayemmnrdlflvs	10800

ID	Accession	Protein	Location/Qualifiers
QY	1021	GATKGIQRDRQPFILTEHFMTVIRSGKSVQNSHELQKFTLCEAVEVMMNNRDLFVS	1080
Db	1081	1ftlmajmelpelstckadldhklkllfcngeskearkffagiyeeafngswsctkmwlf	1140
QY	1081	1FTLMJGMELEPSTCKADLDHLKTLFCNGESKEARKFFAGIYEAFNGSWSTKTNLWF	1140
Db	1141	havkhy 1146	
QY	1141	HAVKHY 1146	
RESULT 2			
ID	R46294	standard; Protein; 1068 AA.	
AC	R46294		
DT	17-AUG-1994	(first entry)	
DE	Ptdins 3-kinase 110 kD catalytic subunit.		
KW	110 kD catalytic subunit; phosphatidylinositol 3-kinase; transformation; schizosaccharomyces pombe; nmt promoter; thiamine; ptdins 3-kinase assay; detection; cell growth; regulation; cancer; blood vessel plaques.		
KM	Bos taurus.		
OS	Bos taurus.		
FH	Key	Location/Qualifiers	
FT	peptide	163..175	
FT	peptide	/note="peptide A"	
FT	peptide	326..337	
FT	peptide	/note="peptide B"	
FT	peptide	441..464	
FT	peptide	/note="peptide C"	
FT	peptide	622..648	
FT	peptide	/note="peptide D"	
FT	peptide	657..672	
FT	peptide	/note="peptide E"	
FT	peptide	679..699	
FT	peptide	/note="peptide F"	
FT	peptide	712..720	
FT	peptide	/note="peptide G"	
FT	peptide	868..882	
FT	peptide	/note="peptide H"	
FT	peptide	885..908	
FT	peptide	/note="peptide I"	
FT	peptide	925..941	
FT	peptide	/note="peptide J"	
FT	peptide	949..966	
FT	peptide	/note="peptide K"	
FT	peptide	987..1010	
FT	peptide	/note="peptide L"	
FT	peptide	1031..1040	
FT	peptide	/note="peptide M"	
FT	peptide	1055..1063	
FT	peptide	/note="peptide N"	
PN	W09403609-A.		
PD	17-FEB-1994.		
PF	05-AUG-1993; G01651.		
PR	05-AUG-1992; GB-016654.		
PA	(IMCR) IMPERIAL CANCER RES TECHNOLOGY.		
PI	Goode NT, Nurse PM, Parker PJ, Waterfield MD;		
DR	WPI; 94-065697/08.		
DR	N-PEDB; 057012.		
PT	Eukaryotic cells transformed with mammalian phospholipid or		
PT	protein kinase DNA - useful in assays for compounds involved in		
PT	cell growth regulation and for treating cancers		
PS	Disclosure; Fig 1; 71pp; English.		
CC	This sequence represents the 110 kD catalytic subunit of the		
CC	phosphatidylinositol (Ptdins) 3-kinase. The cDNA encoding this		
CC	sequence was transformed into Schizosaccharomyces pombe cells under		
CC	the regulatory control of the nmt promoter in an embodiment of the		
CC	invention. In the presence of thiamine the promoter is inactive and		
CC	the cells carrying the ptdins catalytic subunit plasmid grow as the		
CC	parental strain. In the absence of thiamine the nmt promoter functions		
CC	and the ptdins 3-kinase catalytic subunit is induced. Ptdins activity		
CC	is substantially increased under these conditions. Cells containing		
CC	constructs such as this, are useful in assays for detecting compounds		
CC	involved in cell growth regulation. It is also used as the basis for		


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QY 964 TQMKRYFESVDRLFCVGVSVATYIMGIRKDRSDMLTLEDGKYVHIDFGHILGKRT 1023
Db 944 kfygkrerpyfvtlqgdflliviskgaecctreferefcemcykaylatirhanlfnlfs 1003
QY 1024 KLCIQDRQPFILTEHFMVIRSGKSVDSNHELQKFKTLCEVAEYEMMNRRDLFVSLFT 1083
Db 1004 mmllgsgmpelqsfddlaylrlktl-aldktegealeymkqmdahbggtctmdwifhlt 1062
QY 1084 LMLGMEIPELSTRADLDHLKTKTLFCNGESKEERARFFAGIYEAFNGSMSTKTNMLEHAV 1143
Db 1063 kg 1064
QY 1144 KH 1145

RESULT 4
AC R43342 standard; Protein; 1068 AA.
DE 12-APR-1994 (first entry)
DI Human p110.
KW Phosphoinositide kinase; PI; p85 subunit; screening; agonist;
  antagonist; cell proliferation; inhibition; prophylaxis; therapy;
  platelets; neutrophil activity; 3-phosphorylated phosphoinositides.
OS Human.
FH Key Location/Qualifiers
FT domain 19..100
FT note= "binds with p85 subunit"
PN W09321328-A.
PN 28-OCT-1993.
PR 13-APR-1992; GB-008135.
PR 13-APR-1992; GB-008135.
PA (LUDW-) LUWIG INST CANCER RES.
PI Dhand R, Fry MJ, Gout I, Hiles ID, Otsu M, Panayotou G;
  PI Parterp, Volinia S, Waterfield MD;
  DR MPI: 93-351738/44.
  DR N-PSDB: Q51156.
PT Recombinant polypeptide(s) - with phosphoinositide-3 kinase
  activity, useful for controlling cell proliferation
PS Claln 24; Fig 16; 146pp; English.
CC Southern blot analysis was performed using a bovine cDNA probe contg.
  a fragment of a PI3-kinase-encoding sequence and human cDNA isolated
  from a cDNA library constructed from mRNA isolated from the human
  cell line KG1a. Positive clones were sequenced to give the human
  PI3 kinase p110 sequence. This sequence has 95 percent homology
  with the bovine sequence. The domain contg. residues 19-100 of human
  CC p110 is sufficient to associate with the p85 kinase subunit. The
  CC protein with PI3 kinase activity is useful for screening for
  CC (antagonists of PI3 kinase activity which could be useful for
  CC stimulation or inhibition of cell proliferation and hence
  CC prophylaxis or therapy. Platelet or neutrophil activity or blood
  CC glucose levels can be controlled using the kinase.
  CC See also R43341 and R46552-3.
SQ Sequence 1068 AA;

Query Match 13.4%; Score 1151; DB 8; Length 1068;
Best Local Similarity 30.7%; Pred. No. 4.35e-88;
Matches 240; Conservative 211; Mismatches 267; Indels 64; Gaps 41;

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QY 552 HRSTWETLIMDDY--BSCIRDEYKKLQMLVKKNHSGVILEDEQVMMRRYIOK 609
Db 561 -lpeilpkll-lsvknsrdevaemcykdwprlpkpegamelldeonypdmvrgfavrc 618
QY 610 QEPDILLIVSELAFVMTDENFSELVMEKKKRPVSAALULLGRCRDVIRKAVAK 669
Db 619 lekyltdklsqylqlvavlykyeqyldnllyrfillkaltqrighffwllksee--m 675
QY 670 LNEOLSPVTFHFLPLILALKEPRPOSEVGMMILTRALCYRIGHRLFWMLEIARL 729
Db 676 hn---ktve-grfgllleaycracgmylklhlnvyeamkllnldllqetkdeqkq 731
QY 730 RQDDLKSEERYRISLMEAYIRKGENEHKIIITRQYDMVDLIRISTLVGMPEDAV--T- 786
Db 732 mkflveqmrtpdfmdalqglspinpahqignrlrkecrimsakrplwvneopdimse 791
QY 787 MK-LRDEL-R-S-ISHKEMENDSPLDVPYRLGEMIIIDKALVALOSAKRPLMLHKNKPKSD 843
Db 792 llfgnneilfkngddlrqdmlltqltrmenlwqngldlrmlygclsldgcvglllev 851
QY 844 LHLPCAMIFKMGDDLRQDMVLQYLEVANDNWKANIDCCINPYAVLPMGEMIGIIEVY 903
Db 852 rnshtlmqgckg-ikgslg-fnshtlnqvl-k-----d-kng--ely-da-a--ld- 895
QY 904 PNCKTIFETIQVGTGFNMTAVRSTIDPEFNKWKIRKOCIGIDEXKSKSDTKPIEKIDN 963
Db 896 ---l--f-t--r--scagycvatflllgdrhnsnlnwkddqqlfhdffghlkhkk 943
QY 964 TQMKRYFESVDRLFCVGVSVATYIMGIRKDRSDMLTLEDGKYVHIDFGHILGKRT 1023
Db 944 kfygkrerpyfvtlqgdflliviskgaecctreferefcemcykaylatirhanlfnlfs 1003
QY 1024 KLCIQDRQPFILTEHFMVIRSGKSVDSNHELQKFKTLCEVAEYEMMNRRDLFVSLFT 1083
Db 1004 mmllgsgmpelqsfddlaylrlktl-aldktegealeymkqmdahbggtctmdwifhlt 1062
QY 1084 LMLGMEIPELSTRADLDHLKTKTLFCNGESKEERARFFAGIYEAFNGSMSTKTNMLEHAV 1143
Db 1063 kg 1064
QY 1144 KH 1145

RESULT 5
AC W90083 standard; Protein; 1102 AA.
DE 09-MAR-1999 (first entry)
DI Porcine G-protein regulated p130 adapter subunit protein.
KW Phosphoinositide 3-hydroxylase; PI3; trimeric G protein; porcine;
  adapter subunit; regulatory subunit; p101; p120; catalytic subunit;
  detection; diagnosis; activation disorder; haematopoietic system;
  treatment; immune disorder; inflammation; arthritis; septic shock;
  adult respiratory distress syndrome; pneumonia; asthma; allergy;
  reperfusion injury; atherosclerosis; Alzheimer's disease; cancer.
OS Sus. scrofa.
PN US5856132-A.
PN 05-JAN-1999.
PR 15-AUG-1997; 916917.
PR 15-AUG-1997; US-916917.
PR 27-JUN-1996; US-672211.
PA (ONX-) ONX PHARM.
PI Braselmann S, Hawkin PT, Stephens L;
  DR MPI: 99-105107/09.
  DR N-PSDB: V74100.
PT Nucleic acid encoding regulatory (p101) and catalytic (p120)
  subunits of a heterodimeric phosphatidylinositol-3 kinase - useful
  in treatment and diagnosis of immune system disorders, e.g.
  PT arthritis, cancer and Alzheimer's disease
PS Example IX: Fig 4; 75pp; English.
CC This sequence represents a novel catalytic subunit, p120, from porcine
  CC phosphoinositide 3-hydroxylase (PI3K) which is regulated by beta-gamma
  CC subunits of trimeric G-protein. Nucleic acid coding for p101 or p120, or
  CC their fragments, are used as probes and primers for identifying p101 or

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OY 1127 AFGNSMSTKTNLPHAV 1143

RESULT 11

ID W1576 standard; Protein: 1049 AA.

AC W1576:

DE 25-MAR-1997 (first entry)

DE Human phosphatidylinositol 3-kinase PI3K-gamma.

KM Phosphatidylinositol 3-kinase; gamma; PI3K; Immunogen; immunoassay;

KM cell proliferation; receptor-mediated signal transduction;

KM histamine secretion; nerve cell differentiation; glucose transport;

KM modulation; regulation; Alzheimer's disease; lipolysis.

OS Homo sapiens.

EH Key Location/Qualifiers

FT Peptide 741..755

FT /label= Immunogen

FT /note= "antibodies are pref. raised against this

FT peptide; location given as 741-745 in the

FT claims"

DE4445562-C1.

PD 04-APR-1996.

PD 20-DEC-1994; 445562.

PR 13-OCT-1994; DE-436696.

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PI Hanck T, Stoyanov B, Wetzker R;

DR WPI: 96-172545/18.

DR N-PSDB: T58545.

PT New phosphatidylinositol 3-kinase protein - useful as immunogen and

PT for determ. of kinase activity

PS Claim 1: Page -: 10pp; German

CC A 402 bp cDNA fragment was amplified from a human bone marrow

CC library using PCR primers corresponding to amino acid sequences

CC KNGDNR and HIDEF. The amplified fragment was used to probe a human

CC U937 cell cDNA library and several overlapping clones were isolated.

CC The largest clone had a sequence coding for a protein having the

CC present sequence of 1049 residues. The protein is a novel

CC phosphatidylinositol 3-kinase (PI3K) that differs in its regulatory

CC mechanism from the known PI3K-alpha and -beta enzymes. The new enzyme

CC has been designated PI3K-gamma and can be used as an immunogen. The

CC enzyme, antibodies against it or nucleic acid encoding it can be used

CC for modulating cell proliferation, receptor-mediated signal

CC transmission, histamine secretion, nerve cell differentiation, glucose

CC transport and anti-lipolytic activity or for treating Alzheimer's

CC disease.

CC N.B. Although the claimed sequences are referred to by SEQ.ID.

CC Number, a sequence listing did not appear in the original printed

CC patent application.

CC Sequence 1049 AA;

SO

Query Match 10.7%; Score 925; DB 20; Length 1049;

Best Local Similarity 33.1%; Pred. No. 6,52e-68;

Matches 216; Conservative 171; Mismatches 204; Indels 62; Gaps 31;

DB 429 VLLIILDHFLIRGEYVIMMGISQGE-DGSGFNADLTATAPDKE-NSMSISLID 486

OY 482 VMSLTLDMWDELRLGOOFELHMAPEPTANRSRIGENGARIGNAATITISYCGRVNRP 541

DB 487 nychlalpbkqpt-pdp-e--gdyraempqlrkqlaalat-dplnplaeedkellw 541

OY 542 SOGQTYLVKHSRTWTETINIMGDYESIRPGYKKLQMLYKKNHSGVLEDEDEBRHW 601

DB 542 hfr-yeslhpkyakplfs-svkwwgqelvaktyqlaarevdgaaldvqltmqliden 599

OY 602 MRRRIYQKQEPDLTLYLSELAFVMTDRENFSELYVLEK--WKPSVAALIT--LLGR 656

DB 600 fsdenvralavklesleddvhl-yllqlvgavkfeypndaalafllkrglnkrish 658

OY 657 CTDRIYIRKRAVEKLNEQLSPVTFHFLIDPLIALKKEPRAQSGVGMILLRLACDRIH 716

DB 659 flfwfirseiaagryh---qg--rfavlleayllrgcgfahmdftgvgvlemqlkv 712

OY 717 RLFWLLRAIALRLROCDLKSEYRIRISLMEAYLRG-NNEHKITIRROYDMDDELTRIST 775

DB 713 dkslsaeekyvsqvisqlkxklenlqnsqjpsesfrvypqplkagalaiekckymask 772

OY 776 LVKMP--K-DVAT--M-KLDELRSISH-KM-ENMSSPDPVYKLGMIITDKAIVLSA 827

DB 773 kkp1wlefcadpta-lanetigilfkpgddlrqdmlllqilrimeswetesldlclp 831

OY 828 KRPMLHKKNNKPKSDLLPFCAMTFKNGDDLRODMVLQVLEVMNDNTRKANAIDCCINP 887

DB 832 ygcistgdklmlelvkadtiaikqstv-gntg--afkdevlnhwl-k-----ek-- 879

OY 888 YAVLEPMGEMIGIEVVPCKITFEIQVCTGFMTNRAVRSIDSPFMKIRKOCIEDEKK 947

DB 880 ----s----pteekf---ga-----averfyscaagvatfviglgdrhndmltctg 923

OY 948 SKRDSFKNPFEKIDNTGAMKRYESVDFLYSCVGSVATYIMGIRKSHSDNMLTLEDG 1007

DB 924 nlhfdghlignvysfignkerpffvltqdfvwm--gtsgkxtspbfkfgdlcvka 981

OY 1008 KVMIDFGHILGHGKTGKIGIOROPFILTHERFMTVINSGRSVDSNHELQFKTLCEVA 1067

DB 982 ylalrhnlllflsmnlmtgmpqltskedyleyldal-tvqkneadakyf 1033

OY 1068 YEVMNNNDLFSVLTMLGHELPSTKADLDHLKTLFCNGSEKSEARKEFF 1120

RESULT 12

ID W1577 standard; Protein: 1050 AA.

AC W1577:

DE 25-MAR-1997 (first entry)

DE Human phosphatidylinositol 3-kinase PI3K-gamma.

KM Phosphatidylinositol 3-kinase; gamma; PI3K; Immunogen; immunoassay;

KM cell proliferation; receptor-mediated signal transduction;

KM histamine secretion; nerve cell differentiation; glucose transport;

KM modulation; regulation; Alzheimer's disease; lipolysis.

OS Homo sapiens.

EH Key Location/Qualifiers

FT Peptide 742..756

FT /label= Immunogen

FT /note= "antibodies are pref. raised against this

FT peptide; location given as 742-746 in the

FT claims"

DE4445562-C1.

PD 04-APR-1996.

PD 20-DEC-1994; 445562.

PR 13-OCT-1994; DE-436696.

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PI Hanck T, Stoyanov B, Wetzker R;

DR WPI: 96-172545/18.

DR N-PSDB: T58546.

PT New phosphatidylinositol 3-kinase protein - useful as immunogen and

PT for determ. of kinase activity

PS Claim 1: Page -: 10pp; German

CC A 402 bp cDNA fragment was amplified from a human bone marrow

CC library using PCR primers corresponding to amino acid sequences

CC KNGDNR and HIDEF. The amplified fragment was used to probe a human

CC U937 cell cDNA library and several overlapping clones were isolated.

CC The largest clone coded for a protein of 1049 residues. The protein

CC is a novel phosphatidylinositol 3-kinase (PI3K) that differs in its

CC regulatory mechanism from the known PI3K-alpha and -beta enzymes.

CC The new enzyme has been designated PI3K-gamma. Another clone, coding

CC for a PI3K-gamma having the present sequence of 1050 residues, was

CC then isolated. The enzyme can be used as an immunogen. The enzyme,

CC antibodies against it or nucleic acid encoding it can be used

CC for modulating cell proliferation, receptor-mediated signal

CC transmission, histamine secretion, nerve cell differentiation,

CC glucose transport and anti-lipolytic activity or for treating

CC Alzheimer's disease.

CC N.B. Although the claimed sequences are referred to by SEQ.ID.

CC Number, a sequence listing did not appear in the original printed

CC patent application.

CC Sequence 1050 AA;

SO

Query Match 10.7%; Score 925; DB 20; Length 1050;

Best Local Similarity 33.1%; Pred. No. 6,52e-68;
Matches 216; Conservative 171; Mismatches 204; Indels 62; Gaps 31;

Db	430	vn11idbrflrrgrryvlhmwqdsygcg--dgsfnadk1tstpnkce-nms1s11ld	487
Oy	482	vnmscltdrdelrkgoflflhmladepfannsr1gcenar1gtaav1telst5ggvrrnp	541
Db	488	nuchpialpkhqpc-rpbr-e--gdrtvaempnqlrkqleaiat-dplnpltaedkellw	542
Oy	542	sogqytvlvkrhrrswteltlnimbdyesc1rbdgcykklqvlvkkhsgivleedbrnhw	601
Db	543	hfr-yeslknphkayprlfs-svkvgqgeivaktqqlarrevwdsqalavltmq1lscn	600
Oy	602	mmrrr1qkoqeedlltvlse1afvwtddrense1vymlek---wkppsaaalt--llgkr	656
Db	601	fsgdenvra1avqk1lesieddv1h-ylllqvavkvfepnydsalafll1krg1nkr1sh	659
Oy	657	ctdv1rkrfv1aek1neolspvteflhflrplqlaktyerpaos5vgnml1tralcdr1st	716
Db	660	flwflf1se1a1sg1hy-----qg--rfav1leay1rgcg1aml1dfc1gqv1em1q1vcl	713
Oy	717	rlfvl1lre1rlr1ldcd1k1sefyr1sl1meat1lrg-neh1k1t1tr1ov1md1el1r1st	775
Db	714	d1ks1l1se1kv1d1ss1qv1sq1k1k1le1n1qns1q1bes1f1rv1py1dp1k1aga1a1ek1ck1ym1sk	773
Oy	776	lvk1gmp--k-dvat--m-klr1del1rs1sh--km-enn1ds1pl1dp1v1yk1gem11dr1k1avl1gsa	827
Db	774	kkp1w1ek1ec1d1p1a-1sne1t1g1fl1fh1g1dd1l1q1dm1l1q1l1l1me1se1e1d1cl1p	832
Oy	828	kr1p1ml1h1m1k1n1p1r1sd1h1l1p1f1c1a1f1n1g1d1l1r1d1m1l1v1o1l1v1m1n1i1w1a1n1i1d1c1l1p	887
Db	833	yg1sc1st1g1d1k1me1a1v1d1act1a1k1q1st1v-gnt1y--afk1dev1dn1w1-k-----ek--	880
Oy	888	yavl1p1m1g1em1c1i1e1lv1n1c1k1t1f1e1t1o1g1c1g1f1m1t1r1a1v1s1d1p1s1m1n1k1r1k1o1c1s1e1d1e1k1k	947
Db	881	----s-----ptee1k1f-----ga-----aver1f1vs1ca1g1c1v1a1f1l1g1d1r1h1n1d1im1t1e1t1g	924
Oy	948	sk1k1st1k1p1e1r1k1d1n1t1o1q1a1m1k1k1y1e1s1d1r1l1y1s1c1v1s1v1a1t1y1m1g1k1d1r1s1d1m1l1t1e1d1g	1000
Db	925	n1h1f1d1f1h1l1g1n1y1k1s1f1l1g1n1k1e1v1r1p1d1f1f1m--gt1sg1k1t1es1p1h1q1k1d1q1c1v1a	982
Oy	1008	ky1v1d1e1h1l1g1h1g1k1t1g1k1g1o1r1d1o1p1l1t1e1h1m1t1v1r1s1g1s1v1d1g1n1s1h1e1l1o1k1f1t1c1v1a	1067
Db	983	y1a1l1r1h1t1n1l1l1l1f1s1m1l1m1t1g1m1q1l1s1k1e1d1e1y1d1a1-t1v1g1k1ne1d1ak1y1f	1034
Oy	1068	ky1v1w1m1n1n1d1f1v1s1l1f1t1m1l1g1h1e1l1p1e1l1s1t1k1a1d1h1k1t1l1c1n1e1s1k1e1a1r1k1f	1120
RESULT 13			
ID	W38756	standard; Protein; 1726 AA.	
AC	W38756;		
DT	22-JUN-1998	(first entry)	
DE	Phosphatidyl inositol 3-kinase cdk-m.		
KW	Phosphatidyl inositol 3-kinase; signal transduction; cell cycle; antagonistic; inflammatory joint disease; cell proliferation; cancer; psoriasis; restenosis; atherosclerosis; therapy; diagnosis; mouse;		
KW	cdk-m.		
OS	Mus musculus.		
FX	Key	Location/Qualifiers	
FT	Protein	69..1726	
FT		/note- "Claim 5"	
FT	Peptide	391..404	
FT		/note- "Claim 10"	
FT	Misc_difference	941	
FT		/note- "encoded by TAY"	
FT	Domain	1590..1726	
FT		/note- "C2 domain"	
FT	Domain	1175..1345	
FT		/note- "catalytic domain"	
PN	MO9731650-A1.		
PD	04-SEP-1997.		
PR	12-FEB-1997; U02193.		
PR	29-FEB-1996; U5-609049.		

PA (REGC) UNIV CALIFORNIA.
PI Chen Y, Molz L, Williams LT;
DR WPI; 97-448442/41.
DR N-PSDB; T80199.

ID	W70991 standard: Protein: 1686 AA.	Query Match	Best Local Similarity	Matches	Score	DB	Length
		7.0%;	30.1%;	172;	599;	29;	1726;
		Conservative	137;	Mismatches	210;	Indels	52;
				Gaps	35;		
Db	914	KLIDILHR-DASGFSKEDKVFLEWNYGOLKH-PNOLPKLASAP-NWK-WANLAKTYS	969				
Qy	578	KLOMLYKKNHESGIVLEBEDQRHVMKRRYIOKQEPD-LVLVSLASLAVWTDREKFSLLYV	636				
Db	970	LIHWPIPLCIPLAELIIDAKFADGQVSVLAVSW-N-EAISDDELADLLPGFVALKYEYL	1028				
Qy	637	MLEKMKPPSVAAALTLTGKCRCTDRVIRKFAERKNEQLSPYFHLFILPQIALKTEPRA	696				
Db	1029	NSSLVFIILSTRALNQLAHSLYALK-D-A-IHDTIFGR-YENHIGALLSVGGKILRE	1084				
Qy	697	QSEGMMLLTALCDYRGHRLFLAEALRLDCDLKSEEVNRI-SLIMEAYLRRNEE	755				
Db	1085	ELSKGMKIVGLIGGVAAEKVSGASTGCVVLAQKMERGVSFILR-NKCRIPDKPSLVAKE	1143				
Qy	756	HIKITRQVWDVDELIRTRSTLYKMKPRDVAITMKRLDELRSISAKMEMNDSPLDPVYRLGE	815				
Db	1144	INIKSCSFSSANPLKYVTWNAQPIGE-ELN-VM-FKYGEDIRGMLAQLMKLMDK	1199				
Qy	816	MIIDKAIYVGSARKPRMLMHMKNNKPKSDHLHPCFAMIFKNNDLRODMVLQYVLEVDNI	875				
Db	1200	WLKEGLDITMWYIFCISLTGTRGMVELYPAASDLIRKIQVEYG-VTGSFKD-KP-LAEWL	1255				
Qy	876	WKANINDCINLPYAVLWPGEMIGILTEVAPNCKITFEIYGVGFENITVVRSIDSPFNKRWI	935				
Db	1256	IK-Y-NP---S-E-----E---EY-E-K--AS-ENIFYSCAGCAATYILGCD	1290				
Qy	936	RKCGIEDBEKKRSKKSDSKNPTEIKKIDNTQAMKRYFESSVDRELFSCGYSVATYIMIKD	995				
Db	1291	RHNDLMLRSTGLMFIHIDFGKFLIGHAQ-MFGSKFIRDAPIYLTSD-MAYVING-GEKPT	1347				
Qy	996	RHSDMLMTEDGKRVYHIDFGHILGHGKTKLG-IORDROPFILTEHFMTVIRSGKSVGNS	1054				
Db	1348	R-FGLFVDELCCGAYNLIKQGNILFINLISLMPSGDELICSLGDKLYVTALQPT-TDA	1405				
Qy	1055	HELDKFKTLCEAEVMMNNRDLFVSFTLMLGNELEPSTKALDLHKRTLCNGESKE	1114				
Db	1406	EATLIFTRLIESSL-GSIATKFNFIIMLQ	1435				
Qy	1115	EARKFAGIYEDAFNGSWSTKTNMLFPAVKH	1145				

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Db 502 RELGFNTSYAGLSNRIRADNRELSDEKQALACTRDPLESLTEOEKD-FLMSRHHCYN 560
QY 553 RS-TWETELNMGDDY--ESCIRDPGYKKLOMLYKKNHESGIVLEDEQRHVMRRRYIOK 609
Db 561 T-PEILPEKL-LSVKNMSRDEVAQMYCLVNDMPPIKEQAMLEDCNPDPMVAVRVC 618
QY 610 QEPDLILVLSLAVWTDRENSELYVMEKMKPPSVAALTLGLKCTDRIYIKFAVEK 669
Db 619 LEKYLTDKLSQYLLOLVQVLYEQLDNLQVRLFKKALTNRIGHEFFHMLKSE--M 675
QY 670 LNEGLSPVTFHLPLPLIOALKEPRAQSEVGMMLTFRALCDYRIGHLEFLMLAEIARL 729
Db 676 HN--KTVS--QRFGLLESYCRACGMVYKLSRQVEAMEKILNTDLIOEKDETOKVQ 731
QY 730 RDCDLKSEERYRISLMEAYLRGNEEHKITTQVDVDELTRISTLYVKGMPKQVA--T- 786
Db 732 MKFLVEQMRPDEMDALOGFISPLNPAHQGLNLEECRIMSSAKRPLMLNMPDIME 791
QY 787 MK-LRDEL-R-S-ISHKKNENDSPLDPYKLGEMITDKAIVLGSAKRPLMLNKNPKSD 843
Db 792 LLFONNELIFKNGDDLRODMLTLOIRIMENIMONOGDLMLPYGCLSIGCVGLEEV 851
QY 844 LHLFCAMIFKNGDDLRODMLVQVLEVMONIKRANIDCOLNPAVLPNGEMIGIIEV 903
Db 852 RSSHTIMOIOCKG-LKGALO-FNSHTLHOWL-K-----D-KNKG--E--MY--DAID- 895
QY 904 PNCRTIFEIOVGTFMTAVRSIDPSEFMKNWIRKOCGIEDEKSKSKDSTKNPIEKKIDN 963
Db 896 ---L--F-T--R--SCAGYVATFLIGDRHNSINWMDQGLFHDGHFLDKKK 943
QY 964 TOAMKKFFESVDRFLYSCVGSVATYIMGIDKDRSDNMLMTEGKYVHIDGHILGHKT 1023
Db 944 KFGYKRRVFPVLTQDLIIVISGAOECTRTREFEPOEMCYKAYLAIROHANFLINFS 1003
QY 1024 KLGIORROPFILLTEHMTVIRSGKSVDSHLOKFKTLCVEAYEVMMNNRDLFVSLFT 1083
Db 1004 MMLGSGPELOSPPDIAYIKRTL-ALDKTEQALEYFMKQMNDAHGGWTKMDWITHTI 1062
QY 1084 LMLGMEPELSTKADLDHLKTLFCNGESKEEARKFFAGIYEAFNGSWSSTKTNMLPHAV 1143
Db 1063 KO 1064
QY 1144 KH 1145

RESULT 2
AC 039483 PRELIMINARY; PRT: 1083 AA.
AC 039483;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE GAG-V-PHOSPHINOSITIDE 3-KINASE CATALYTIC SUBUNIT FUSION PROTEIN (FRAGMENT).
DE GAG-V-P3K.
GN AVIAN SARCOMA VIRUS 16
OS AVIAN SARCOMA VIRUS 16
OC VIRUSES; RETROID VIRUSES; RETROVIRIDAE; AVIAN TYPE C RETROVIRUSES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97334438.
RA CHANG H.W., AOKI M., FRUMAN D., AUGER R.R., BELLACOSA A.,
RA TSICHGIS P.N., CANTLEY L.C., ROBERTS T.M., VOST P.K.;
RT "Transformation of chicken cells by the gene encoding the catalytic
RT subunit of p13-kinase."
RL SCIENCE 276:1848-1850(1997).
DR EMBL: AF001075; G2245503; -.
DR PRAM: PF000454; P13.P14.kinase: 1.
DR PRAM: PF000613; P13Ka: 1.
DR PRAM: PF00792; P13K.C2: 1.
DR PRAM: PF00794; P13K.Tbd: 1.
FT NON_TER 1
SQ SEQUENCE 1083 AA; 125869 MW; F0D9D1C3 CRC32;
Query Match 13.5%; Score 1165; DB 14; Length 1083;

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Best Local Similarity 30.6%; Pred. No. 1,27e-200;
Matches 239; Conservative 212; Mismatches 267; Indels 64; Gaps 40;
Db 341 SLMTINSALRIR-ILCTAYVNVIRIDIKRYVRT--GIYGGPELDDNVTOFVPSNPR 397
QY 385 SLMDLDANLIRRVNISGF-DPPA-DVD-MYVIESVYVIGITLTLAK-STTVYNAQFAK 440
Db 398 WN-EWLSYDMYIPDLPPAARLCLISYVGRKGAKEHCEPLANGINIMEDYDTLVSGKM 456
QY 441 WNKEMYTFDLYMKDMPESA-V-LSIRVLGYKVLKSEEFYGVWNSLTDWRDELQOGQ 498
Db 457 ALNINAVPHGLEDLNPIGTVGSPNPKGTPCLELEFDMSPNPKFPMYIEEHAMWIS 516
QY 499 LPHLMA-PEPTAR-SKIGENGARIGTNA-VRIEISSYGRVRRMPSQ--QYTLVKN 552
Db 517 RELGFNTSYAGLSNRIRADNRELSDEKQALACTRDPLESLTEOEKD-FLMSRHHCYN 575
QY 553 RS-TWETELNMGDDY--ESCIRDPGYKKLOMLYKKNHESGIVLEDEQRHVMRRRYIOK 609
Db 576 T-PEILPEKL-LSVKNMSRDEVAQMYCLVNDMPPIKEQAMLEDCNPDPMVAVRVC 633
QY 610 QEPDLILVLSLAVWTDRENSELYVMEKMKPPSVAALTLGLKCTDRIYIKFAVEK 669
Db 634 LEKYLTDKLSQYLLOLVQVLYEQLDNLQVRLFKKALTNRIGHEFFHMLKSE--M 650
QY 670 LNEGLSPVTFHLPLPLIOALKEPRAQSEVGMMLTFRALCDYRIGHLEFLMLAEIARL 729
Db 691 HN--KTVS--QRFGLLESYCRACGMVYKLSRQVEAMEKILNTDLIOEKDETOKVQ 746
QY 730 RDCDLKSEERYRISLMEAYLRGNEEHKITTQVDVDELTRISTLYVKGMPKQVA--T- 786
Db 747 MKFLVEQMRPDEMDALOGFISPLNPAHQGLNLEECRIMSSAKRPLMLNMPDIME 806
QY 787 MK-LRDEL-R-S-ISHKKNENDSPLDPYKLGEMITDKAIVLGSAKRPLMLNKNPKSD 843
Db 807 LLFONNELIFKNGDDLRODMLTLOIRIMENIMONOGDLMLPYGCLSIGCVGLEEV 866
QY 844 LHLFCAMIFKNGDDLRODMLVQVLEVMONIKRANIDCOLNPAVLPNGEMIGIIEV 903
Db 867 RSSHTIMOIOCKG-LKGALO-FNSHTLHOWL-K-----D-KNKG--E--MY--DAID- 910
QY 904 PNCRTIFEIOVGTFMTAVRSIDPSEFMKNWIRKOCGIEDEKSKSKDSTKNPIEKKIDN 963
Db 911 ---L--F-T--R--SCAGYVATFLIGDRHNSINWMDQGLFHDGHFLDKKK 958
QY 964 TOAMKKFFESVDRFLYSCVGSVATYIMGIDKDRSDNMLMTEGKYVHIDGHILGHKT 1023
Db 959 KFGYKRRVFPVLTQDLIIVISGAOECTRTREFEPOEMCYKAYLAIROHANFLINFS 1018
QY 1024 KLGIORROPFILLTEHMTVIRSGKSVDSHLOKFKTLCVEAYEVMMNNRDLFVSLFT 1083
Db 1019 MMLGSGPELOSPPDIAYIKRTL-ALDKTEQALEYFMKQMNDAHGGWTKMDWITHTI 1077
QY 1084 LMLGMEPELSTKADLDHLKTLFCNGESKEEARKFFAGIYEAFNGSWSSTKTNMLPHAV 1143
Db 1078 KO 1079
QY 1144 KH 1145

RESULT 3
AC P91634 PRELIMINARY; PRT: 1088 AA.
AC P91634;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PHOSPHINOSITIDE 3-KINASE, DP110.
DE DROSOPHILA MELANOGASTER (FRUIT FLY).
OS EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
OC PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
OC DROSOPHILIDAE; DROSOPHILA.
RN [1]
RP SEQUENCE FROM N.A.

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RESULT      8
ID 061182      PRELIMINARY;      PRT: 1658 AA.
AC 061182;
DT 01-NOV-1996 (TREMBLREL, 01, CREATED)
DT 01-NOV-1996 (TREMBLREL, 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL, 08, LAST ANNOTATION UPDATE)
DE PHOSPHATIDYLINOSITOL 3-KINASE, C2 DOMAIN CONTAINING, ALPHA
DE POLYPEPTIDE (PHOSPHOINOSITIDE 3-KINASE).
GN PIK3C2A OR CPK-M.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA.
OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB C;
RC MEDLINE; 96278630.
RA MOLEZ L.M., CHEN Y.W., HIRANO M., WILLIAMS L.T.;
RT "Cpk is a novel class of Drosophila Ptdins 3-kinase containing a C2
RT domain".
RL J. BIOL. CHEM. 271:13892-13899(1996).
DR EMBL; U52193; GI272422; -.
MGD; MG1:1203729; PIK3C2A.

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RESULT	9	PRELIMINARY;	PRT;	76 AA.
ID	017482			
AC	017482;			
DT	01-NOV-1996 (TREMBL.REL. 01, CREATED)			
DT	01-NOV-1996 (TREMBL.REL. 01, LAST SEQUENCE UPDATE)			
DT	01-JAN-1999 (TREMBL.REL. 03, LAST ANNOTATION UPDATE)			
DE	AGE-1 PROTEIN (FRAGMENT).			
GN	AGE-1.			
OS	CAENORHABDITIS ELEGANS.			
OC	EUDAROTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;			
OC	RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELIODIRINAE; CAENORHABDITIS.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	SWINBURNE J.;			
RL	SUBMITTED (OCT-1995) TO EMBL/GENBANK/DBJ DATA BANKS.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 94150718.			
RA	WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,			
RA	BONFIELD J., BUTTON J., CONNELL M., COSEY T., COOPER J., COULSON A.,			

RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIKKEN L., ROOPRA A., SAUNDERS D., SHONKKEEN R.,
 RA SMAILDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL NATURE 368:32-38(1994).
 DR EMBL: Z66519; E1343409; .
 FT NON_TER 1 1
 SQ SEQUENCE 76 AA; 8935 MW; D3CD53C2 CRC32;

Query Match 6.88; Score 582; DB 5; Length 76;
 Best Local Similarity 100.0%; Pred. No. 5.16e-83;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MNRRDLFVSLFTLMGMLPELSTKADLDLKLTLFCNGESKEARKFEAGIYEAFNG 60
 |||||
 Qy 1071 MNRRDLFVSLFTLMGMLPELSTKADLDLKLTLFCNGESKEARKFEAGIYEAFNG 1130
 |||||
 Db 61 SWSTKTNMLFHAVKH 76
 |||||
 Qy 1131 SWSTKTNMLFHAVKH 1146

RESULT 10
 ID 075747; PRELIMINARY; PRT; 1448 AA.
 AC 075747;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE P13-KINASE.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN -[1]
 RP SEQUENCE FROM N.A.
 RA ROZCYKA M., BROWN R., FRX M.;
 RT "cDNA cloning of a novel mammalian p13-kinase."
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ000008; E1309758; .
 SQ SEQUENCE 1448 AA; 166094 MW; D96DE697 CRC32;

Query Match 6.88; Score 590; DB 4; Length 1448;
 Best Local Similarity 28.9%; Pred. No. 1.40e-84;
 Matches 165; Conservative 146; Mismatches 211; Indels 49; Gaps 31;

Db 655 KH1ARLSOKO-TPLLSEKKRYLWFRFYCNNECSLPVLGSAP-GMDR-TVSEMT 711
 |||||
 Qy 577 KRLQMLVKKHESGIVLEEDQRHVMWMMRYIOKEPDLIVLSLAFVWTDRENSLY 636
 |||||
 Db 712 ILRRWFSQPLALGLTTSFPDOETRKVAVOQDLNDELLE-YLPOLVQKFEWNL 770
 |||||
 Qy 637 MEKMKPSPVAALTLGKRCIDRVIRKFAVEKLNQSLPVTFLPLIQALKEPRA 696
 |||||
 Db 771 ESQLVOLLHRSLSQIQAARLWYLLK-N-AE-NEAVFKSM-YOKLLAALQFCAGALND 826
 |||||
 Qy 697 QSEVGMMLTRALCDYRIGRLFWLRAETARLRDCLDSEERYRRLSLMEAVL-KNEE 755
 |||||
 Db 827 EFSKEOKLILKIDIGERSASDHOEVLAKKEI-GRLEEFQDVTCHLPINPALCIR 885
 |||||
 Qy 756 HIIITROYDMDVDELTRISTLVKGMKPDVATMKINDELSLSHKKNMDSPLDPYKIGE 814
 |||||
 Db 886 GIDHDCSFTSNAALPLKTFINANLGMK-NI---SIIIFAGDLDRLMDLVLDLQVMDN 941
 |||||
 Qy 815 EMIDIAIVGSAKRPLMLMKNNKPKSDHLRPFCAIIFKNGDLDRLMDLVLDLQVMDN 874
 |||||
 Db 942 IWIQEGIDMQMIIRYRCSTGKDRIVQMDVATLAKIHHSGSLG-PLK-ENT-IKKY 997
 |||||
 Qy 875 IMAANIDCCLNPAVALPKEMIGILLEVVPNCCTIFEIOVGTFMTAVRSIDPSEMNK 934

Db 998 FS-Q--HNHLK-A-D---Y--EK-----ALRN-F-----F-YSCAGCVTEILGVC 1032
 |||||
 Qy 935 IRQGIIEDEKKSKSDSKNPKLEKKIDNTQAMKYFESVDPLFVSCVGSVATYIMGK 994
 |||||
 Db 1033 DRANDNIMLTGKSHMHIDFGKFLGHAOTFGGKIKDRAPFITSE-MEFTITE-GGK-NP 1089
 |||||
 Qy 995 DRSDMDMLTEDEGKYVHIDFGHILGKTKLGIORDRPFILTEHMTYIRSGKSVDGNS 1054
 |||||
 Db 1090 OHFODEVEELCCRAYNIIRKSQLNLNLEMLYAGLPESLGIQDKYVYNNLRPO-DTDL 1148
 |||||
 Qy 1055 HELQKTKTLCVARYEVMWNNRDLFVSLFTLMGMLPELSTKADLDLKLTLFCNGESNE 1114
 |||||
 Db 1149 EATSHFTKKIKESLE-CFEPVKLNMLIHTLAQ 1178
 |||||
 Qy 1115 EARKFEAGIYEAFNGSMSTKTNMLFHAVKH 1145

RESULT 11
 ID 061194; PRELIMINARY; PRT; 1509 AA.
 AC 061194;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE PHOSPHATIDYLINOSITOL 3-KINASE, C2 DOMAIN CONTAINING, ALPHA
 DE POLYPEPTIDE (P170 PHOSPHATIDYLINOSITOL 3-KINASE).
 GN PIK3C2A.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 OC SCIROGNATHI; MORIDAE; MORINAE; MOS.
 RN -[1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96278746.
 RA VIRASITUS J.V., GUILHERME A., CZECH M.P.;
 RT "Mouse p170 is a novel phosphatidylinositol 3-kinase containing a C2
 RT domain."
 RL J. BIOL. CHEM. 271:13304-13307(1996).
 DR EMBL: U55772; G1305538; .
 DR MGD: MGI:1203729; PIK3C2A.
 DR PFAM: PF00168; C2; 1.
 DR PFAM: PF00454; P13_P14_kinase; 1.
 DR PFAM: PF00613; P13Ka.1.
 DR PFAM: PF00787; PX; 1.
 DR PFAM: PF00792; P13K_C2; 1.
 DR PFAM: PF00794; P13K_Ibd; 1.
 SQ SEQUENCE 1509 AA; 170777 MW; E404092B CRC32;

Query Match 6.88; Score 589; DB 11; Length 1509;
 Best Local Similarity 30.5%; Pred. No. 2.20e-84;
 Matches 174; Conservative 136; Mismatches 207; Indels 54; Gaps 33;

Db 699 KLDLIIHR-DSSFGSKDEKVFLEWERYCYLKH-PCPLKPIIASAP-MNK-WANLAKTVS 754
 |||||
 Qy 578 KLOMLVKKHESGIVLEEDQRHVMWMMRYIOKEPDLIVLSLAFVWTDRENSLY 636
 |||||
 Db 755 LHWMPPLCPALBELLDKAFADQEVRSILAVSM-EAISDELADLDLPOVALYEIYL 813
 |||||
 Qy 637 MEKMKPSPVAALTLGKRCIDRVIRKFAVEKLNQSLPVTFLPLIQALKEPRA 696
 |||||
 Db 814 NSLSVFLSLRAGLQINQASHSLWYLLK-D-A-LHDTGFSR-YEHYGLALLSVGGKGLRE 869
 |||||
 Qy 697 QSEVGMMLTRALCDYRIGRLFWLRAETARLRDCLDSEERYRRL-SLMEAVYRGNKE 755
 |||||
 Db 870 ELSKOMKLVOLLGGAVEKVRQASGSROYVLDKSMERVOSEFLR-NKCLPLKPSLVAKE 928
 |||||
 Qy 756 HIIITROYDMDVDELTRISTLVKGMKPDVATMKINDELSLSHKKNMDSPLDPYKIGE 815
 |||||
 Db 929 LNIKSCSFSSNAMPKVTVMNADPLGE-EIN-YV-FKVGEDLDRLMDLALQIMIKIMKI 984
 |||||
 Qy 816 MIIDKAIIVGSAKRPLMLMKNNKPKSDHLRPFCAIIFKNGDLDRLMDLVLDLQVMDN 875
 |||||
 Db 985 WLKESGIDLRVIFRCLSTGRGQWELVPAASDTLRKIOVEYV-VYSGSLRK--PT--SEWL 1039
 |||||

QY 876 WAAAIIDCCLNPAVLPMEGMIIEVVPNCKTIFEIOVGTFMNTAVRSIDPSFNKMT 935
 Db 1040 RK-----N--NPSEE--EY-E--K--AS-ENFIYSCAGCCVATVYLIGD 1074
 QY 936 RKQCIIEDEKKSKSDSTNPIEKKIDNTQAMKKYFESVDRLYSVGSVATYIMGID 995
 Db 1075 RHNDNIMLRSTGHMFHIDFGKFLGHAQ-MGSEFRDRAFPVLTSD-MAYVING-GEKPTI 1131
 QY 996 RHSDNMLMTEDEKGYVHIDFGHILGHGKTKLG-IORDRQPFILTEHMTVIRSGKSDGN 1054
 Db 1132 R-FOLFVDLCCOAYNLIRFT-NLFLNLISLMIIPSGLPBELTSIODLKVYRDLAQPT-TDA 1188
 QY 1055 HELQKFETLCVATEYVMNNRDLFVSLFTLMGLMELPELSTKADLDHLKTLFCNGESKE 1114
 Db 1189 EAATIEFTRLIESSL-GSIATKNEFFIHNLAQ 1218
 QY 1115 EARKFFAGIYEAFNGSMSTKTNMLFPAVKH 1145

RESULT 12
 ID 000443 PRELIMINARY; PRT; 1686 AA.
 AC 000443;
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE PHOSPHOINOSITIDE 3-KINASE.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97479209.
 RA STEIN R.C., WATERFIELD M.D.;
 RT "Cloning of a human phosphoinositide 3-kinase with a C2 domain that
 displays reduced sensitivity to the inhibitor wortmannin."
 RL BIOCHEM. J. 326:139-147(1997).
 DR EMBL; Y13367; E1188595; -.
 DR PFAM; PF00168; C2; 1.
 DR PFAM; PF00454; P13_P14_kinase; 1.
 DR PFAM; PF00613; P13Ka; 1.
 DR PFAM; PF00787; PK; 1.
 DR PFAM; PF00792; P13K_C2; 1.
 DR PFAM; PF00794; P13K_Ibd; 1.
 SO SEQUENCE 1686 AA; 190736 MW; 8BA83E82 CRC32;

Query Match 6.8%; Score 590; DB 4; Length 1686;
 Best Local Similarity 30.0%; Pred. No. 1,40e-84;
 Matches 175; Conservative 139; Mismatches 204; Indels 54; Gaps 36;

Db 874 KLLDILHK-DSSILGSKEDKAFLEMEKRYCCFKH-PNCLPRLITLAP-NMK-MGNLAKTYS 929
 QY 578 KQMLVKKHESGIVLEEDDRHMMKRIYIQOEPR-LIIVSELAFWTDRENFSELY 636
 Db 930 LHQWPAALPLALLELDSKFADEYRSIAVTWI-EAISDELTDLLPOFVALKYEYL 988
 QY 637 MEKMKPSPVAALTLGKRCTDRVIRKFAVEKLNQOLSPVTFHLPLIQALKEPRA 696
 Db 989 NSLSVFLSLRALGNTQIAHNLWLIK-D-A-LHDVQF-STREHVLGALLSGKRLNE 1044
 QY 697 QSEVGMWLTTRALCDYRIGHRLFWLRAETARLURDCLDSEERYRI-SLMEAYLRGNE 754
 Db 1045 ELIKQ-TKIVOLLGVAENYRQASGAROVYLQBSMERVOSEFOK-NKCLPLKPSLVAK 1102
 QY 755 EHRTITROYDWDDELTRISTLYKGMKPDVATYKLDLDELRSISHKKNENDSPLDPYKKG 814
 Db 1103 ELINIKSCSFSSNAVPLKYTMVADPLGE-EIN-VN-FKVGEDLRODMALOMIMDK 1158
 QY 815 EMLIDKAIYVLSAKRPLMLHMKKNPKSDLHLPFCAMIFKNGDLDQDMVLVQLVEWMDN 874
 Db 1159 IWLKEGLDLRMVTFKCLSTGRDGMVELVPSADTLRKIQVEYG-VIGSEFD-KP-LAEV 1214
 QY 875 IWRANIDCCLNPAVLPMEGMIIEVVPNCKTIFEIOVGTFMNTAVRSIDPSFNKMT 934

Db 1215 LRK-Y--NP--S-E-----EY-E--K--AS-ENFIYSCAGCCVATVYLIG 1249
 QY 935 IRKQCIIEDEKKSKSDSTNPIEKKIDNTQAMKKYFESVDRLYSVGSVATYIMGID 994
 Db 1250 RHNDNIMLRSTGHMFHIDFGKFLGHAQ-MGSEFRDRAFPVLTSD-MAYVING-GEKPTI 1306
 QY 995 RHSDNMLMTEDEKGYVHIDFGHILGHGKTKLG-IORDRQPFILTEHMTVIRSGKSDGN 1053
 Db 1307 IR-FOLFVDLCCOAYNLIRKQTNLFLNLISLMIIPSGLPBELTSIODLKVYRDLAQPT-TD 1364
 QY 1054 SHELQKFETLCVATEYVMNNRDLFVSLFTLMGLMELPELSTKADLDHLKTLFCNGESK 1113
 Db 1365 EAATIEFTRLIESSL-GSIATKNEFFIHNLAQ 1395
 QY 1114 EARKFFAGIYEAFNGSMSTKTNMLFPAVKH 1145

RESULT 13
 ID 024453 PRELIMINARY; PRT; 1876 AA.
 AC 024453;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE PHOSPHOINOSITIDE 3-KINASE.
 GN P13K 68D.
 OS DROSOPHILA MELANOGASTER (FRUIT FLY).
 OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
 OC PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYROIDEA;
 OC DROSOPHILIDAE; DROSOPHILA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96362138.
 RA MACOGUALL I.R., DOMIN J., WATERFIELD M.D.;
 RT "A family of phosphoinositide 3-kinases in Drosophila identifies a
 new mediator of signal transduction."
 RL CURR. BIOL. 5:1404-1415(1995).
 DR EMBL; X92892; E211623; -.
 DR PFAM; PF00168; C2; 1.
 DR PFAM; PF00454; P13_P14_kinase; 1.
 DR PFAM; PF00613; P13Ka; 1.
 DR PFAM; PF00787; PK; 1.
 DR PFAM; PF00792; P13K_C2; 1.
 DR PFAM; PF00794; P13K_Ibd; 1.
 SO SEQUENCE 1876 AA; 210434 MW; 5B720832 CRC32;

Query Match 5.2%; Score 452; DB 5; Length 1876;
 Best Local Similarity 25.2%; Pred. No. 6.65e-58;
 Matches 140; Conservative 146; Mismatches 234; Indels 35; Gaps 32;

Db 1059 ERREYWEKRLYQSPNALPKVLHA-AHSW-DYANLIDLHLLHSMAPLSPLQSLLELL 1116
 QY 596 EQRHV-WMKRRIYIQOEPRLLIYVSELAFWTDRENFSELYMLEKMKPSPVAALITLIG 654
 Db 1117 PRYPDAVREKAVENTS-KMPNDQVDFLPOLVOSIKHDTYGSAMARFLSKCESPRF 1175
 QY 655 KCTQDVIRKFAVEKINQEDLSPVTFHLPLIQLAKYEPRAOSEGMWLTTRALCDYRI 714
 Db 1176 GHMTWLL-VH-S-LPD-D--PHNSIGAAMVDOEIDESOYTOVRYRRNKKMLRALMAIC 1229
 QY 715 GHRLEWLLRAETARLURDCLDSEERYRISLMEAYLRGNEBHIKITROYDWDDELTRIS 774
 Db 1230 G-EKMLQRMVGHKMOCKITIAESVKEAKESMRQSLAAGDEVHODLDEPT-CLPIG 1287
 QY 775 TLVYKMPKQVATYKLDLDELRSISHKKNENDSPLDPYKIGEMIIDKAIYVLSAKRPLMLH 834
 Db 1288 -PELEV-TGVSVRNGS-YF-NSNTPLPKINFGPDAESLPAIFKGGDDLOQDOLITQLIR 1343
 QY 835 WKNKNKPSDLHLPFCAMIFKNGDLDRODM-LVQLVEWMDNIMK-AANIDCCLNPAVLP 892
 Db 1344 IANKMLAERLDLKKYTFNC-VPTGKSGMIELVSEAEFLRK-IQVEGCLTGSFK-DR-- 1398
 QY 893 MEGMIIEVVPNCKTIFEIOVGTFMNTAVRSI-DPSPFNKMKIRKQCIIEDEKKSKSD 951

Db 1230 G-EKMLQRFMYQHRCQKLTITIAESVKEAKESMRQKSLAAGMDEVHODLEOPT-CLPLG 1287
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QY 893 MGEMLGIEVVPNCRTIFEIQGTGFMTAVRSI-DPSFMNWKIRKQCGIEDEKRSKD 951
Db 1399 PIAEWLGR--QNPSPLE-YQSAVRNFTLSCAGYVATYVLCICDRHNDNIMLKTSGHLPH 1455
QY 952 STKNPIEKIDNTQAMKRYFESVDRELYSCVGYVATYIMGIDRHSNDMLTEDGKYVH 1011
Db 1456 IDFGFLGDAQ-MFGNFKRDRTPFVLTSD-MAYVING-G-DKPSIDFHYFVLDCCAFNI 1511
QY 1012 IDFGHILGHGKTKLG-IQRDROPFILTEHFMVIRSGKSVDSNSHELQFKTLCEAEYEV 1070
Db 1512 VRKNADLLHLTAHMATAGMPGVNSNA-VQYVRALL-PSQSNPEAATFAAMIOSLK- 1568
QY 1071 MMNNDLFLVSLFTLMGLMELPELSTKADLDHLKTLFCNGESKEEARKFPAIYEAFNG 1130
Db 1569 SWFTQFNFFLNLAQ 1583
QY 1131 SWSTKTNMLFHAVKH 1145

Search completed: Fri Jul 16 17:08:28 1999
Job time : 74 secs.

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 16, 1999, 20:02:42 ; Search time 66.58 Seconds

(without alignments)
9901.048 Million cell updates/sec

Title: US-08-908-453-2

Perfect score: 3504

Sequence: 1 CGGAGCCATGAGCTGAG.....ACGAGTCGAACTACTGTA 3504

Scoring table: IDENTITY_NUC

Searched: 240622 seqs, 94065609 residues

Database: N.Geneseq_34.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3504	100.0	3504	1	Caenorhabditis ele
2	148	4.2	3498	1	Ptdlns 3-kinase 11
3	146.4	4.2	3207	1	p110 CDNA. Recombi
4	130	3.7	3412	1	Human p110 CDNA. R
5	103.6	3.0	3387	1	CDNA encoding mam
6	103.6	3.0	5220	1	Human phosphatidy
7	96.4	2.8	3808	1	Porcine phosphol
8	86.8	2.5	4134	1	Human phosphatid
9	86.8	2.5	4137	1	Human phosphatid
10	68.6	2.0	5061	1	CDNA encoding a hu
11	65.6	1.9	5285	1	Phosphatidyl inos
12	49.8	1.4	6831	1	Phosphatidyl inos
13	48.8	1.4	381	1	Human P17R-C CDNA.
14	48	1.4	393	1	Human P17R-F CDNA.
15	40.6	1.2	957	1	Aequorin gene Bios
16	38.8	1.1	2100	1	Streptococcus uber
17	37	1.1	4918	1	Sequence of the L.
18	36.8	1.1	110000	1	Continuation (15 o
19	35.6	1.0	1612	1	Sequence encoding f
20	35.2	1.0	731	1	RsaI restriction f
21	34.8	1.0	3602	1	Human NP1K gene. N
22	34.8	1.0	2487	1	Human NP1K gene. N
23	34.8	1.0	3324	1	Human NP1K gene. N
24	34.8	1.0	2451	1	Human NP1K gene. N
25	34.4	1.0	110000	1	Continuation (11 o
26	34	1.0	2652	1	Sequence encoding
27	33.8	1.0	3561	1	Delta endotoxin ge
28	33.8	1.0	3561	1	Bacillus thuringie
29	33.8	1.0	3561	1	Bacillus thuringie
30	33.8	1.0	2821	1	Human cystatin B g
31	33.8	1.0	2821	1	Human mutant EPM1
32	33.8	1.0	3561	1	Nematode toxin 80J
33	33.6	1.0	2418	1	Human brain Expres
34	33.6	1.0	423	1	Plasmodium falcipa
35	33.6	1.0	2663	1	H. pylori secreted
36	33.6	1.0	1131	1	Candida albicans C
37	33.6	1.0	4492	1	Hamster ileal/rena
38	33.4	1.0	2265	1	560E1 CDNA encodin
39	33.4	1.0	2117	1	Human secreted pro
40	33.2	0.9	2369	1	Human secreted plas
41	33.2	0.9	2293	1	CDNA encoding falc
42	33	0.9	2223	1	Plasmodium falcipa
43	33	0.9	2223	1	Plasmodium falcipa

ALIGNMENTS

RESULT	ID	Score	Length	DB ID	Description
1	V18654	100.0	3504	1	Caenorhabditis ele
2	V18654	100.0	3504	1	Caenorhabditis ele
3	V18654	100.0	3504	1	Caenorhabditis ele
4	V18654	100.0	3504	1	Caenorhabditis ele
5	V18654	100.0	3504	1	Caenorhabditis ele
6	V18654	100.0	3504	1	Caenorhabditis ele
7	V18654	100.0	3504	1	Caenorhabditis ele
8	V18654	100.0	3504	1	Caenorhabditis ele
9	V18654	100.0	3504	1	Caenorhabditis ele
10	V18654	100.0	3504	1	Caenorhabditis ele
11	V18654	100.0	3504	1	Caenorhabditis ele
12	V18654	100.0	3504	1	Caenorhabditis ele
13	V18654	100.0	3504	1	Caenorhabditis ele
14	V18654	100.0	3504	1	Caenorhabditis ele
15	V18654	100.0	3504	1	Caenorhabditis ele
16	V18654	100.0	3504	1	Caenorhabditis ele
17	V18654	100.0	3504	1	Caenorhabditis ele
18	V18654	100.0	3504	1	Caenorhabditis ele
19	V18654	100.0	3504	1	Caenorhabditis ele
20	V18654	100.0	3504	1	Caenorhabditis ele
21	V18654	100.0	3504	1	Caenorhabditis ele
22	V18654	100.0	3504	1	Caenorhabditis ele
23	V18654	100.0	3504	1	Caenorhabditis ele
24	V18654	100.0	3504	1	Caenorhabditis ele
25	V18654	100.0	3504	1	Caenorhabditis ele
26	V18654	100.0	3504	1	Caenorhabditis ele
27	V18654	100.0	3504	1	Caenorhabditis ele
28	V18654	100.0	3504	1	Caenorhabditis ele
29	V18654	100.0	3504	1	Caenorhabditis ele
30	V18654	100.0	3504	1	Caenorhabditis ele
31	V18654	100.0	3504	1	Caenorhabditis ele
32	V18654	100.0	3504	1	Caenorhabditis ele
33	V18654	100.0	3504	1	Caenorhabditis ele
34	V18654	100.0	3504	1	Caenorhabditis ele
35	V18654	100.0	3504	1	Caenorhabditis ele
36	V18654	100.0	3504	1	Caenorhabditis ele
37	V18654	100.0	3504	1	Caenorhabditis ele
38	V18654	100.0	3504	1	Caenorhabditis ele
39	V18654	100.0	3504	1	Caenorhabditis ele
40	V18654	100.0	3504	1	Caenorhabditis ele
41	V18654	100.0	3504	1	Caenorhabditis ele
42	V18654	100.0	3504	1	Caenorhabditis ele
43	V18654	100.0	3504	1	Caenorhabditis ele

Db 241 TGGTTCTTGCAGATGCGGACATCGCTAGCAATCAAGCTATCAAGTTCAACATCA 300
Qy 301 CTTTTCGATTTGATTTGCTCCGATGAGTGGGAGACATATTCGTAAGCCAGAGATTAT 360
Db 301 CTTTTCGATTTGATTTGCTCCGATGAGTGGGAGACATATTCGTAAGCCAGAGATTAT 360
Qy 361 GTTTCACACAGCTTGAATTAATTTGGCGCAATTTGAATTATTTAACGAGATCAACC 420
Db 361 GTTTCACACAGCTTGAATTAATTTGGCGCAATTTGAATTATTTAACGAGATCAACC 420
Qy 421 CTGTGCAATTAAGAGCTCCAGCGACCTTCCCAATGCTTTTCTACCAACCTGATGA 480
Db 421 CTGTGCAATTAAGAGCTCCAGCGACCTTCCCAATGCTTTTCTACCAACCTGATGA 480
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Qy 601 AGCAAGAAAGAGCTGCTGACAGCTGAGCTGAGGTACAGTCACTAGCGCTCCGCA 660
Db 601 AGCAAGAAAGAGCTGCTGACAGCTGAGCTGAGGTACAGTCACTAGCGCTCCGCA 660
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Db 661 GAACAGTACTTGTGTGTGTGTGAATCGTCCGAAAGATTTGGAATCAAAAGTCAAGCT 720
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Db 901 GAAGAGTGTCTTCAATTTGGCTGAGTACACAGCTTGTTCACAAATCCAGATCTCAA 960
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Db 1141 AGCAGACCAAAAGAGAGAGAAAGAGAGAGATGATGATGATGATGATGATGATGAT 1200
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Db 1201 TCACCTCAAAAGATTTCACTTTGGAGCTTGAAGCGGAATCTTATGATAGAGCTGAT 1260
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Qy 1981 AAATGGAACCGCGAGTGTGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
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Db 2221 TGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
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Db 2401 ATGCAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460

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DB 2821 AATACAGAGTTCGAGATGATGATCCTTCTTATGAAATAGTGAGATTCGGAACATGTC 2880
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DB 2941 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000
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DB 3361 GATCATTTGGAAGAAACCTCTTCTGCAATGAGAGAAAGCAAGAGAGAGAGAGTTT 3420
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DB 3421 TTCCGTCGAATCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTT 3480
QY 3481 TTCCAGCAGTCAAAACACTACTGA 3504
DB 3481 TTCCAGCAGTCAAAACACTACTGA 3504

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RESULT 2
ID 057012
AC 057012 standard; cDNA to mRNA; 3498 BP.
DE 31-AUG-1994 (first entry)
KW 110 kD catalytic subunit; phosphatidyl inositol 3-kinase;
transformation; Schizosaccharomyces pombe; nmt promoter; thiamine;
KW Ptdins 3-kinase; assay; detection; cell growth; regulation; cancer;
OS blood vessel plaques; ss.
FH Bos taurus.
FT Key location/Qualifiers
FT cds 1..3207
FT /tag- a
FT /product- P110
PN M09403609-A.
PD 17-FEB-1994.
PF 05-AUG-1993; G01651.
PR 05-AUG-1992; GB-016654.
PI (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
PA Goode NT, Nurse PM, Parker PJU, Waterfield MD;
DR WPI: 94-065697/08.
P-PSDB: R46294.
PT Eukaryotic cells transformed with mammalian phospholipid or
PT protein kinase DNA - useful in assays for compounds involved in
PT cell growth regulation and for treating cancers
PS Disclosure: Fig 1; 71pp; English.
CC This sequence encodes the 110 kD catalytic subunit of the phosphatidy
CC inositol (Ptdins) 3-kinase. This sequence was transformed into
CC Schizosaccharomyces pombe cells under the regulatory control of the
CC nmt promoter in an embodiment of the invention. In the presence of
CC thiamine the promoter is inactive and the cells carrying the Ptdins
CC catalytic subunit plasmid grow as the parental strain. In the absence
CC of thiamine the nmt promoter functions and the Ptdins 3-kinase
CC catalytic subunit is induced. Ptdins activity is substantially
CC increased under these conditions. Cells containing constructs such as
CC this, are useful in assays for detecting compounds involved in cell
CC growth regulation. It is also used as the basis for detecting
CC compounds for treating cancers and the formation of blood vessel
CC plaques.
SQ Sequence 3498 BP; 1148 A; 627 C; 721 G; 1002 T;

Query Match 4.2%; Score 148; DB 1; Length 3498;
Best Local Similarity 46.0%; Pred. No. 4e-34;
Matches 724; Conservative 0; Mismatches 760; Indels 90; Gaps 3;

QY 1924 CTCGCATTTGTGTGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1983
DB 1924 CTCGCATTTGTGTGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1983
QY 1708 CTGCTGTGTTAATGAACTAGAGATGAAAGTACCTCAGATGATGCTTGTGTAAGAT 1767
DB 1708 CTGCTGTGTTAATGAACTAGAGATGAAAGTACCTCAGATGATGCTTGTGTAAGAT 1767
QY 1984 TGGAAACCCCGAGTGTGGCGACCGCGTTGACTTGTGTAAGAACTTGCACGAGATCGT 2043
DB 1984 TGGAAACCCCGAGTGTGGCGACCGCGTTGACTTGTGTAAGAACTTGCACGAGATCGT 2043
QY 1768 TGGCCTCCAAATCAACCTGAAACAGCTATGAGAGCTTGTGAGCTCAATTAACGATCCT 1827
DB 1768 TGGCCTCCAAATCAACCTGAAACAGCTATGAGAGCTTGTGAGCTCAATTAACGATCCT 1827
QY 2044 GTGATTCGGAAGTTTGCAGTGTGAGAGATGATGATGATGATGATGATGATGATGATGAT 2103
DB 2044 GTGATTCGGAAGTTTGCAGTGTGAGAGATGATGATGATGATGATGATGATGATGATGAT 2103
QY 1828 ATGCTTGTGAGAGTTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 1887
DB 1828 ATGCTTGTGAGAGTTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 1887
QY 2104 CTTTTCATATGCTCTCTCATACAGCGCTTGAATGACAGCCGCTGCTCAATCGGAAGTT 2163
DB 2104 CTTTTCATATGCTCTCTCATACAGCGCTTGAATGACAGCCGCTGCTCAATCGGAAGTT 2163
QY 1888 CAGTACCTTAATTCAGTAGTAGTACAGTACTAATAATATGACAGTATTTGGATTAACCTGCTT 1947
DB 1888 CAGTACCTTAATTCAGTAGTAGTACAGTACTAATAATATGACAGTATTTGGATTAACCTGCTT 1947
QY 2164 GGAATGATGCTCTTGACTAGAGCTCTCTGCATATATGAAATGACATGACATTTTCTG 2223
DB 2164 GGAATGATGCTCTTGACTAGAGCTCTCTGCATATATGAAATGACATGACATTTTCTG 2223
QY 1948 GTGAGATTTTATCAAAAAAGCGTTAATATGAAAGAGAGGCTACTTTTCTTTTGG 2007
DB 1948 GTGAGATTTTATCAAAAAAGCGTTAATATGAAAGAGAGGCTACTTTTCTTTTGG 2007
QY 2224 CTGCTCCGTCGAGAGATGCTGCTTGTGAGAGATGATGATGATGATGATGATGATGATGATGAT 2283
DB 2224 CTGCTCCGTCGAGAGATGCTGCTTGTGAGAGATGATGATGATGATGATGATGATGATGATGAT 2283
QY 2008 CATTTAAATCTGAGATGACAAATTAAGACAGTATGCTAGAGAGTTTGGCTGCTTTTGGAG 2067
DB 2008 CATTTAAATCTGAGATGACAAATTAAGACAGTATGCTAGAGAGTTTGGCTGCTTTTGGAG 2067
QY 2284 CGTATCTCAGTCTGATGAGAGCTTACCTCCGTGGAATGAGACACATCAAGATCATC 2343
DB 2284 CGTATCTCAGTCTGATGAGAGCTTACCTCCGTGGAATGAGACACATCAAGATCATC 2343

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Db 2068 TCCATTGCCGTCATGTCGATGATATCTGAGCACTTAATAGCAATTGAGGCTATG 2127
QY 2344 ACCGACAGATTGACATGGTTGATGAGCTCAGACAAATCAGACTCTGTGCAAGATG 2403
Db 2128 GAAAGATCATTAAGTACTGACTGATCTCAACAGAGAGAGAGAGAGAGAGAGAGAG 2187
QY 2404 CCAAAAGATGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2463
Db 2188 GTACAGATGAGATTTTATGTTGA---GCAAAATGGGGGACAGATTTTATGAGCTCTC 2244
QY 2464 GAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2523
Db 2245 CAGGCTTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2304
QY 2524 GCCATCTCTCTAGGAGATGCAAAAGTCCTGTTAAATGCTTCACTGAGAGACAAATCCA 2583
Db 2305 TGTGCAATTAATGCTCTGCAAAAGGCACTGTGTTGAATGGAGAACCCAGACATC 2364
QY 2584 AAGAGTACCTGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2643
Db 2365 ATGTCAGAAATTAACCTTCTCAACAAATGATGATGATGATGATGATGATGATGATG 2424
QY 2644 CAGGACATGCTTGTCTCAAGTCTCTGCAAGTATGATGATGATGATGATGATGATGATG 2703
Db 2425 CAGATATGCTTAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2484
QY 2704 ATGATGCTGTTTGAACCCGTCAGCAGTCTCTCAATGGAGAAATGATGATGATGATG 2763
Db 2485 CTGATCTGCAATGATTAACCTTATGATGATGATGATGATGATGATGATGATGATGATG 2544
QY 2764 GAATTTGCTTATGTTGTAACCAATATGCAATGATGATGATGATGATGATGATGATGATG 2823
Db 2545 GAGGTGATGAGAAATTTCTCAACATATGATGATGATGATGATGATGATGATGATGATG 2598
QY 2824 ACAGCATGTCGAGTATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2883
Db 2598 ----- 2598
QY 2884 ATGAGATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2943
Db 2598 -----GAAAGTGCACCTGACATTTAAACCCAGACACCTCTCACTGAGTGG 2640
QY 2944 ATGATATATCTCAAGCATGAGAAATATTTTGAAGTGTGCTGATCTTACTGCG 3003
Db 2641 CTCAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2700
QY 3004 TGTGTCGATATTCAGTTCGACATGATGATGATGATGATGATGATGATGATGATGATGAT 3063
Db 2701 TGTGTCGATATTCAGTTCGACATGATGATGATGATGATGATGATGATGATGATGATGAT 2760
QY 3064 CTGATGTCACAGATGAGAAATATGTCACATGATGATGATGATGATGATGATGATGATG 3123
Db 2761 ATCATGCTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2820
QY 3124 GGAAGAGCAAACTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3183
Db 2821 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTC 2880
QY 3184 ATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3243
Db 2881 TTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2940
QY 3244 AAAAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3303
Db 2941 CAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3000
QY 3304 TTGTCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3363
Db 3001 CTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060
QY 3364 CATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTC 3423
Db 3061 TACATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTC 3117

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QY 3424 GCTGGAATCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3483
Db 3118 ATGAAACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3177
QY 3484 CAGGAGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3497
Db 3178 CACACCAATTAAGCA 3191

RESULT 3
O51155
ID O51155 standard; cDNA; 3207 BP.
AC O51155;
DT 12-APR-1994 (first entry)
DE p110 cDNA.
KW Phosphoinositide kinase; PI; p85 subunit; screening; agonist;
KW antagonist; cell proliferation; inhibition; prophylaxis; therapy;
KW platelets; neurophil activity; 3-phosphorylated phosphoinositides;
KW ss.
FH Key Location/Qualifiers
cds 1..3207
FT 1.3207
FT /tag= a
FT /note= "PI3- kinase p110"
PN MO9321328-A.
PD 28-OCT-1993.
PR 13-APR-1993; G00761.
PR 13-APR-1992; GB-008135.
PA (LUDWIG-) LUDWIG INST CANCER RES.
PI Dhand R, Fry MJ, Gout I, Hiles ID, Otsu M, Panayotou G;
PI Parker PJ, Volinia S, Waterfield MD;
DR WPI: 93-351738/44.
DR P-PSDB: R43341.
PT Recombinant polypeptide(s) - with phosphoinositide-3 kinase
PT activity, useful for controlling cell proliferation
PS claim 7; Fig 9; 146pp. English.
CC Southern blot analysis was performed using a bovine cDNA probe contg.
CC a fragment of a PI3-kinase encoding sequence and human cDNA isolated
CC from a cDNA library constructed from mRNA isolated from the human
CC cell line K562. Positive clones were sequenced to give the human
CC PI3 kinase p110 sequence shown. This sequence has 95 percent
CC homology with the bovine sequence. The domain encoding residues 19-
CC 100 of human p110 is sufficient to encode the kinase which will
CC associate with the p85 kinase subunit. The gene may be used to
CC provide a protein with PI3 kinase activity, and is useful for
CC screening for (ant)agonists of PI3 kinase activity which could be
CC useful for stimulation or inhibition of cell proliferation and hence
CC prophylaxis or therapy. Platelet or neutrophil activity or blood
CC glucose levels can be controlled using the kinase.
CC See also O51156, O59012-23 and O57522-3.
SQ Sequence 3207 BP; 1028 A; 581 C; 680 G; 918 T;

Query Match 4.2%; Score 146.4; DB 1; Length 3207;
Best Local Similarity 45.9%; Pred. No. 1.1e-33;
Matches 723; Conservative 0; Mismatches 761; Indels 90; Gaps 3;

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QY 2164 GGAATGATGCTCTTACTAGACCTCTCTGCGATTCGATTTGGACATGCTTTTCTGG 2223
 DB 1948 GTGAAATTTTCTCTCAAAAAGCGTTAACTAACTAAAGAGATGCTGCTTTCTTTTGG 2007
 QY 2224 CTGCTCCGTCAGAGATCTCGTTTGAGATGATGATCTGAAAAGTAAATATGCG 2283
 DB 2008 CATTAAATCTGAGATGACATTAACAGATTAGTCAAGTTGGCTCTTTGGAG 2067
 QY 2284 CATTATCTCACTCTGATGAGACCTTACCTCCGTGAAATGAAAGACATCAAGATATC 2343
 DB 2068 TCCATATGCGCGATGATGAGATGATGATGAGACACCTTAATAGCAATTTGAGCTATG 2127
 QY 2344 ACCCGCAAGTTGACATGCTGATGAGCTCACACGATCAGACATCTTGTCAAAGATG 2403
 DB 2128 GAAAAGCTATTACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2187
 QY 2404 CCAAAAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2463
 DB 2188 GTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2244
 QY 2464 GAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2523
 DB 2245 CAGGGCTTCT 2304
 QY 2524 GCGATGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2583
 DB 2305 TGTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2364
 QY 2584 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2643
 DB 2365 ATGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2424
 QY 2644 CAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2703
 DB 2425 CAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2484
 QY 2704 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2763
 DB 2485 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2544
 QY 2764 GAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2823
 DB 2545 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2598
 QY 2824 ACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2883
 DB 2598 ----- 2598
 QY 2884 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2943
 DB 2598 ----- 2640
 QY 2944 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3003
 DB 2641 CTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2700
 QY 3004 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3063
 DB 2701 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2760
 QY 3064 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3123
 DB 2761 ATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2820
 QY 3124 GGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3183
 DB 2821 AAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2880
 QY 3184 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3243
 DB 2881 TTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2940
 QY 3244 AAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3303

DB 2941 CAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3000
 QY 3304 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3363
 DB 3001 CTTTCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060
 QY 3364 CATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3423
 DB 3061 TACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3117
 QY 3424 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3483
 DB 3118 ATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3177
 QY 3484 CAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3497
 DB 3178 CACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3191

RESULT 4
 OS1156
 ID OS1156 standard; cDNA; 3412 bp.
 AC OS1156;
 DT 12-APR-1994 (first entry)
 DE Human p110 cDNA.
 KW Phosphoinositide kinase; PI; p85 subunit; screening; agonist;
 KW antagonist; cell proliferation; inhibition; prophylaxis; therapy;
 KW platelets; neutrophil activity; 3-phosphorylated phosphoinositides;
 KW ds.
 OS Human.
 FH key
 FT cds
 FT 1.3207
 FT /note="PI3-kinase p110"
 PN W09321328-A.
 PD 28-OCT-1993.
 PF 13-APR-1993; G00761.
 PR 13-APR-1992; GB-008135.
 PA (LUDM-) LUDMIG INST CANCER RES.
 PI Dhand R, Fry MJ, Gout I, Hiles ID, Otsu M, Panayotou G;
 PI Parker PJ, Volinia S, Waterfield MD;
 DR WPI; 93-351738/44.
 DR P-PSDB: R43342.
 PT Recombinant polypeptide(s) - with phosphoinositide-3 kinase
 PT activity, useful for controlling cell proliferation
 PS Claim 7; Fig 16; 140pp: English.
 CC Southern blot analysis was performed using a bovine cDNA probe contg.
 CC a fragment of a PI3-kinase-encoding sequence and human cDNA isolated
 CC from a cDNA library constructed from mRNA isolated from the human
 CC cell line K562. Positive clones were sequenced to give the human
 CC PI3 kinase p110 sequence shown. This sequence has 95 percent
 CC homology with the bovine sequence. The domain encoding residues 19-
 CC 100 of human p110 is sufficient to encode the kinase which will
 CC associate with the p85 kinase subunit. The gene may be used to
 CC screening for (antagonists of PI3 kinase activity, and is useful for
 CC useful for stimulation or inhibition of cell proliferation and hence
 CC prophylaxis or therapy. Platelet or neutrophil activity or blood
 CC glucose levels can be controlled using the kinase.
 CC See also OS1155 and OS1522-3.
 SQ Sequence 3412 bp; 1128 A; 616 C; 706 G; 962 T;

Query Match 3.7%; Score 130; DB 1; Length 3412;
 Best Local Similarity 45.7%; Pred. No. 9.8e-29;
 Matches 719; Conservative 0; Mismatches 765; Indels 90; Gaps 4;

QY 1924 CTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1983
 DB 1708 CTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1767
 QY 1984 TGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2043

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Db 1768 TGGCTCCATCAAACTGTAAGAGCTGATGAACTTGTGAGTGAATTAATCCAGATCTT 1827
Oy 2044 GTGATTCGAAAGTTTGACAGTGAAGTGAATGAGCAGCTGAGCCGGTCACTTCAT 2103
Db 1828 ATGGTTGAGGTTTGTCTGTGTGGTCTTGAAAAATATTAAACAGATGACAACTTCT 1887
Oy 2104 CTTTTCATATGCTCTCTCATACAGCGGTGAAGTACGAACCCGCTGCTCAATCGAAGT 2163
Db 1888 CAGTATTTATTCAGCTAGTACAGGCTCTAAATATGAACATATTGTGATTAACCTGCT 1947
Oy 2164 GGAATGAGCTCTTGTACTGATGAGCTCTCTGCAATATTCGAATGAGCATGCTTTCTG 2223
Db 1948 GTGAAATTTTAACTGAAGAAACATTGACTTAATCAAGGATGGGCTCTTTCTTTGG 2007
Oy 2224 CTGCTCCGTCGAGATGCTGTTGAGATGATGATCTGAAAAGTGAAGATATGCG 2283
Db 2008 CATTTAAATCTGAGATGACATTAACAGATTAGCCAGAGGTTTGGCTGCTTTGGAG 2067
Oy 2284 CGTATCTACTTCTGATGAGAGCTTACCTCCGTGAAATGAAGACATCAAGATCATC 2343
Db 2068 TCCATTGTCGTCAGTGGAGATGATTTGAAGCACCTGATAGCAAGTCAGAGCAATG 2127
Oy 2344 ACCGCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2403
Db 2128 GAAAGCTCATTAATTAATCAATTCATCAACAGAGAGAGAGAGAGAGAGAGAGAGAG 2187
Oy 2404 CCAAAAGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2463
Db 2188 GTAC-AGATGAAGTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 2244
Oy 2464 GAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2523
Db 2245 CAGGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2304
Oy 2524 GCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2583
Db 2305 TGTGATATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2364
Oy 2384 AAGATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2643
Db 2365 ATGTAGAGTTACTGTTTGAACAATGATGATGATGATGATGATGATGATGATGATGAT 2424
Oy 2644 CAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2703
Db 2425 CAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2484
Oy 2704 ATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2763
Db 2485 CTTGATCTTCTGATGCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2544
Oy 2764 GAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2823
Db 2545 GAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2598
Oy 2824 ACAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2883
Db 2598 ----- 2598
Oy 2884 ATTGAAGATGAAGAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAG 2943
Db 2598 -----GAAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640
Oy 2944 ATTGAATTAATCAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3003
Db 2641 CTCAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2700
Oy 3004 TGTGTTGATTAATCAAGTTCAGATCAATGATGATGATGATGATGATGATGATGATGAT 3063
Db 2701 TGTGTTGATTAATCAAGTTCAGATCAATGATGATGATGATGATGATGATGATGATGAT 2760
Oy 3064 CTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3123

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Db 2761 ATCATGTTGAAGAGCATGCAACTGTTTCAATATAGATTTTGCACACTTTTGATCAC 2820
Oy 3124 GGAAGACCAAACTTGGATCCAGAGATGCTCAACCTTTATTTCTAAGCAACACTTT 3183
Db 2821 AAGAGAAATAATTTGTTATTAAGAGACAGTGTGCCATTTGTTTGACACAGATTTTC 2880
Oy 3184 ATGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3243
Db 2881 TTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2940
Oy 3244 AAAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3303
Db 2941 CAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
Oy 3304 TGTTCACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3363
Db 3001 CTTTCTCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
Oy 3364 CATTTGAAGAAACCTCTTCTGCAATGAGAGAAAGCAAGAGAGAGAGAGAGAGAGAG 3423
Db 3061 TACATTCGAAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3117
Oy 3424 GCTGATCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3483
Db 3118 ATGAAGCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3177
Oy 3484 CACGAGTCAACA 3497
Db 3178 CACACATTAACA 3191

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RESULT 5
V16533
ID V16533 standard; cDNA; 3387 bp.
AC V16533:
DT 22-JUN-1998 (first entry)
DE cDNA encoding mammalian novel class I p13 kinase designated p110-delta.
KW Autophosphorylation; p13; phosphatidylinositol 3-hydroxy; kinase;
KW activity; p110-delta; melanoma; lipid kinase; metastase;
KW phosphoinositide specificity; regulation; diagnosis; motility;
OS Homo sapiens.
FH Key
FT CDS 1..3387
ET /tag= a
PM WO9746688-A1.
PD 11-DEC-1997.
PR 30-MAY-1997; G01471.
PA (LUDW-) LODWIG INST CANCER RES.
PI Vanhasebroeck B, Waterfield MD;
DR WPI; 98-042196/04.
DR P-PSD3; W46625.
PT Auto-phosphorylating peptide with phosphatidylinositol
PT 3-kinase-like activity, designated p110delta - useful for
PT controlling cell motility, particularly of metastatic cancer cells
PS Disclosure; Fig 9; 72pp; English.
CC The present sequence encodes a novel autophosphorylating protein
CC that has p13 (phosphatidylinositol 3-hydroxy) kinase activity, and
CC is designated p110-delta. The protein is expressed selectively in
CC white blood cells and melanomas. The protein is a lipid kinase with
CC broad phosphoinositide specificity and specific tissue localisation,
CC possibly involved in regulation of melanoma metastases (it is not
CC expressed in normal melanocytes). Fragments of the present
CC sequence are used to detect tissue-specific expression, and a
CC similar analysis can be done at the protein level using antibodies in
CC standard immunoassays. These assays are particularly used for diagnosing
CC and predicting motility/invasiveness of metastatic cancer cells. The
CC protein can be used in human or veterinary medicine for controlling
CC motility of cells, where the protein increases motility while antisense
CC sequences are used to reduce it.
SQ Sequence 3387 bp; 711 A; 1044 C; 1001 G; 631 T;

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Query Match	3.0%;	Score 103.6;	DB 1;	Length 3387;
Best Local Similarity	53.7%;	Pred. No. 8e-21;		
Matches 264;	Conservative 0;	Mismatches 219;	Indels 9;	Gaps 2

QY	3000	CTTGTGTTGGAAATTCACATTCGCGACGACATTAATGGAATCAAGAGATCGACAGTGA	3059
Db	2631	CTCTGTGCTGGCTATTGTGTGGCCACATATGTGCTGGGCATTGGCGATCGGCACAGCGA	2690
QY	3060	TAAATCATGATCTCACTGAGAGATGGAAATAATGTCCACATGTGATTTCCGTACATTTTGGG	3119
Db	2691	CAACATCATGATCCGAGAGAGTGGCGACGCTGCCACATGTGATTTTGGCCACTTCTGTGGG	2750
QY	3120	ACACGGAAAGACCAACTTGGGATTCACAGGAGATGCTAACCGGTTATTTCTAACGGACA	3179
Db	2751	GAAATTCACACCAAGTTTGGATTCACACCGCGCGCGCTGCCATTCATCTCACTACACGA	2810
QY	3180	CTTTATGACAGTGAATTCGATCGAGGTAAATCTGTGATGGAAATTCGCATGACCTCAAAA	3239
Db	2811	CTTTGTGCATGTATTCAGCAGGGGAAA-----GACTAATTAATAGAGAAATTTTGACG	2864
QY	3240	AATCAAAAGCTTAATGCGTGCACACCAACGAAAGTAATGTGGAAATTAATCCAGATTTTGGT	3299
Db	2865	GTTTCGGGGCTACTGTAAGAAAGGCTCTACACCATCTGCGCGGCCACAGGGCTTCTTCTCT	2924
QY	3300	TTCCTTGTACCTTGATGCTCGGAATGAGATGTGCTGAGCTGTGCGACAAAGCCGATTT	3359
Db	2925	CCACCTCTTTGCCCTGATGGGGCGCGACAGGCGCTGAGCTCAGCTGTCTCAAGACAT	2984
QY	3360	GGATCATTTTAAAGAAAACCTCTTCTGTGCATGAGAAACCAAGAAAGAGCGAGAACTT	3419
Db	2985	CCAAATCATCTAAGAGACTCCC---TGCACTGGGGAAAACAGAGGAGAGACACTGAACA	3041
QY	3420	TTTGGCTGGAATCTACGAAAGACCTTCAATGATCATGATCTGTACCAAAACCAATTTGGCT	3479
Db	3042	CTTCGAGTGAAGTTTAACGAAGCCCTCGGTAGAGCTGTGAAACCAAGTAACCTGGCT	3103
QY	3480	CTTCCAGCAGCT	3491
Db	3102	GGCCCAACAGCT	3113

RESULT	6
CC	V131340
CC	V131340 standard; cDNA; 5220 BP.
AC	V131340;
DT	12-OCT-1998 (first entry)
DE	Human phosphatidylinositol 3-kinase p110 delta subunit cDNA.
KM	Phosphatidylinositol 3-kinase; p110 delta; human; immune system;
KW	carcinogenesis; diagnosis; ss.
OS	Homo sapiens.
FX	Key
FT	CDS
FT	Location/Qualifiers
FT	196..3330
FT	/*tag= a
PN	MO9823760-A1.
PD	04-JUN-1998.
PE	25-NOV-1997; U21655.
PR	25-NOV-1996; US-777405.
PA	(ICOS-) ICOS CORP.
PI	Chantry DH, Hoekstra MF, Holtzman DA;
DR	WPI; 98-322736/28.
DR	P-PSDB; W58570.
PT	New phosphatidylinositol 3-kinase catalytic subunit - used to
PT	develop products for modulating kinase activity in immune system
PT	signaling and in carcinogenesis
PS	Claim 4; Page 27-33; 53pp; English.
CC	This full-length composite cDNA encodes the p110 delta catalytic
CC	subunit (see W58570) of human phosphatidylinositol 3-kinase. It
CC	was assembled from clone #249 obtained by PCR amplification (see
CC	V13141-44) of human peripheral blood mononuclear cell cDNA, clone
CC	M928 obtained by screening a human macrophage cDNA library, and
CC	further clones obtained by RACE and PCR (see V13145-50). The
CC	following are claimed: (1) a purified and isolated polynucleotide

CC (PN) encoding p110 delta : (2) a vector comprising a DNA as in (1);
CC (3) a host cell stably transformed or transfected with a DNA as in
CC (1); (4) PN encoding a lipid kinase, and hybridizing to PN having
CC the 5220 bp sequence; (5) a purified and isolated p110 delta
CC polypeptide as in (4); (6) an antibody specifically immunoreactive
CC with p110 delta; (7) a hybridoma cell line (especially 208F
CC (HB 12200) producing a monoclonal antibody as in (6); and (8) a
CC humanized antibody as in (6). p110 delta has kinase activity and
CC may play a role in PI 3-kinase mediated signaling in the immune
CC system and in carcinogenesis. The products can be used to develop
CC agents that modulating p110 delta kinase activity and to develop
CC diagnostic reagents (claimed). They may also be used for detection
CC and diagnosis of p110 delta in a biological sample.
SQ Sequence 5220 BP; 1120 A; 1525 C; 1483 G; 1092 T;

Query Match	3.0%;	Score 103.6;	DB 1;	Length 5220;
Best Local Similarity	53.7%;	Pred. No. 1e-20;		
Matches 264;	Conservative	0;	Mismatches 219;	Indels 9;
				Gaps 2

OY	3000	CTTGTGGTGGAAATTCATCTATGCTCCAGACGTAACATAAAGGGAATCAAGAGATCGCAACAGTA	3059
Db	2826	CTTCCTGGCTGGCGATTGTTGGCCACATATATGCTGGGCATTTGGCGATTCGGCACAGGA	2885
OY	3060	TATATCATGCTCACTCAATGAMATGGAAAAATATGTCACATATGATTTGGGTCACATTTTGGG	3119
Db	2886	CAATATCATATGATCCGAGAGAGATGGGCAAGCTGTTCCATATGATTTTGGCCACTTTTCTGG	2945
OY	3120	ACACGAAAGACCAACCTTGGATCCAGCGAGATGCTCAACCGTTATTTCAACGGAACA	3179
Db	2946	GAATTTCAAGACCAAGTTTGGATTCACACGGCGAGCGTGTCCATTCATCTCACTATGA	3005
OY	3180	CTTATATGACAGTATTTGCATCGGGTAAATCTGTGGATGGAAATTCGCATGACTCAAAA	3238
Db	3006	CTTTGTCCATATGATATCAGCAGCGGAAA-----GACTAATAATAGTGAAATTTGAAACG	3059
OY	3240	ATTCAAAAGCTAATGGCTGCAACGCTACAGAAAGTAATGTGGAAATATCGAGATTTTGTGT	3299
Db	3060	GTTCCGGGGCTACTGTAAAGGGCTCTACACATCTCGCGGCCACAGGGCTTCTTTCT	3119
OY	3300	TTCCTTTTCACCTTGATGCTCGGAATGAGATGCTGCTGAGCTGTGCAGCAAGACGATTT	3358
Db	3120	CCACCTCTTTGGCCTATATGGGGCGGGCAGGCCCTCGCTGAGCTCACTGTCTCCAAAGACAT	3179
OY	3360	GGATTCATTTGAGAAAAACCTCTTCTGCAATGGAGAAACCAAGAAGACGAGAAATT	3419
Db	3180	CCATATCTCTCAAGACTCCC---TGCCACTGGGGAAAAAGAGAGAGACACTGAACA	3238
OY	3420	TTTGGCTGGATCTACGAAAGAACCTTCAATGATATATGTTACCAAAACGATTTGCT	3479
Db	3227	CTTCCGAGTGAAGTTTAAACAGACCCCTCGTGAGACTGGAAAAACCAAGATGAACTGCT	3299
OY	3480	CTTCACGCAAGT 3491	
Db	3297	GGCCCAACAGCT 3308	

RESULT	7	
ID	V04634	
AC	V04634	
DT	17-AUG-1998	(first entry)
DE	Porcine phosphonositide 3OH-kinase p120 subunit cDNA.	
KW	G-beta-gamma regulated phosphatidylinositol-3' kinase; pig;	
KW	phosphonositide 3OH-kinase; PI3K; signal transduction;	
KW	phosphatidylinositol (3,4,5)-triphosphate; G-protein; receptor	
KW	transgenic animal; knockout animal; inflammation; arthritis;	
KW	septic shock; adult respiratory distress syndrome; pneumonia;	
KW	asthma; allergy; reperfusion injury; atherosclerosis; cancer;	
KW	Alzheimer's disease; cancer; antisense; ribozyme; diagnosis;	
KW	therapy; drug screening; ss.	
OS	Sus scrofa.	
EH	Key	Location/Qualifiers

Db	3253	ATTAAGGAGAGTGCATTGTGTCTTAACCCCTGACTTCTCTTTTGAT	-----GGGAA	3306
Qy	3306	AATCTGGATGGAAATTCGATGACCTACAAAAATTCAAAAGTTATGCGTGAAGCT		3265
Db	3307	CTTCTGGAAAGAAAGACAGACCCACACTTCAGAAATTTGAGACATCTGTGTGAAGCTT		3366
Qy	3366	ACGAGTAATAGTGGAAATATCGAATTTGCTTCCCTGTTCACCTTGATGCTCGGAA		3325
Db	3367	ATCTAGCCCTTTCGTCAACACAAACCTTACTGTACTCTGTTCACATGATGCTGATGA		3426
Qy	3326	TGGAGTGCCTGAGCTGTGCGACCAAGCGAATTTGGATCATTTGAAGAAACCCCTC		3381
Db	3427	CAGGAATGCCCCAGTTTACAGCAAGAAAGAACATTAAATATCCGGGATGCCCTC		3482

RESULT 9

ID		758546 standard; cDNA: 4137 BP.
AC		T58546;
DT	25-MAR-1997 (first entry)	
DE	Human phosphatidylinositol 3-kinase PI3K-gamma cDNA.	
KM	Phosphatidylinositol 3-kinase; gamma; PI3K; immunogen; immunoassay;	
KW	cell proliferation; receptor-mediated signal transmission;	
KW	histamine secretion; nerve cell differentiation; glucose transport;	
KW	modulation; regulation; Alzheimer's disease; lipolysis; ds.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	cds	423..3575
FT	*tag -a	/product=PI3K-gamma
FN		
PN	DE4445562-C1.	
PD	04-APR-1996.	
PF	20-DEC-1994; 445562.	
PR	13-OCT-1994; DE-436696.	
PI	(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.	
PA	Hanck T, Stoyanov B, Wetzel R;	
DR	WPL: 96-172545/18.	
PT	P-PDB: W1577.	
PS	New phosphatidyl-inositol 3-kinase protein - useful as immunogen and	
PT	for determ. of kinase activity.	
PS	Claim 5; Page -: 10pp; German.	
CC	A 402 bp cDNA fragment was amplified from a human bone marrow	
CC	library using PCR primers corresponding to amino acid sequences	
CC	KNGBDIR and HIRFG. The amplified fragment was used to probe a human	
CC	U937 cell cDNA library and several overlapping clones were isolated.	
CC	The largest clone coded for a protein of 1049 residues. The protein	
CC	is a novel phosphatidylinositol 3-kinase (PI3K) that differs in its	
CC	regulatory mechanism from the known PI3K-alpha and -beta enzymes.	
CC	The new enzyme has been designated PI3K-gamma. Another clone, coding	
CC	for a PI3K gamma of 1050 residues and having the present	
CC	sequence, was then isolated. The enzyme can be used as an immunogen.	
CC	The enzyme, antibodies against it or nucleic acid encoding it can be	
CC	used for modulating cell proliferation, receptor-mediated signal	
CC	transmission, histamine secretion, nerve cell differentiation,	
CC	glucose transport and anti-lipolytic activity or for treating	
CC	Alzheimer's disease.	
CC	N.B. Although the claimed sequences are referred to by SEQ.ID.	
CC	Numbers, a sequence listing did not appear in the original printed	
CC	patent application.	
SQ	Sequence 4137 BP:	1127 A; 999 C; 1001 G; 1010 T;
<hr/>		
Query Match	2.5%; Score 86.8; DB 1; Length 4137;	
Best Local Similarity	52.4%; Pred. No. 9,9e-16;	
Matches 218; Conservative	0; Mismatches 192; Indels	6; Gaps
DY	2966 AGAATATTGTTGAAGTCGCATCGCATCTCATAACGCGTGTGGATTCAGTTGCCA 3025	
DB	3076 AAAAGTTTCAGCGACGAGTGAGAGATTTGTTATTCTCTGAGGCTACTGTGGCA 3135	
XY	3026 CGTACATTAATCGAATCAAGATCTGCACAGTAGTAAATTCAGTACGCACTGAAGATGCA 3085	

Db	3136	CCTTGTCTTGGAAATAGGGCAGACACAAATGACATATTTATGATCCACCGAGAGTAA	3195
Qy	3086	AATATGCCACATGATGTTTGGTCACATATTTGGGACACGGAAAGCAACACTGGATGCC	3145
Db	3136	ACATATTTCATATGACTTTGGGCAATCTTGGGATATACAAAAGTTTCCGGGCATTA	3255
Qy	3146	AGCAGATGCTCAACCGTTTATTTCTAACGGAACACTTTATGACAGTGTGATCGGGTA	3205
Db	3256	ATTAAGAGAGAGTGCCTATTTGTCTTAACCCCTGACTCTCTTTGTGAT-----GGGAA	3309
Qy	3206	AATGTGGATGGAAATTCGACATGACCTCAAAAANTTCAAAAGTTATGCTGCAAGCT	3265
Db	3310	CTTCTGGAAAGAACACAGCCACACCTTCAGAAATTCAGACATCTGTGTAAAGCTT	3369
Qy	3266	ACGAAGTAATGTGGAAATATCGAATTTTGTGTTTCCTTGTTACCTGTGATGCTCGGAA	3325
Db	3370	ATCTAGCCCTTCGCATCACACAAACCTACTGATCTCTGTTCTCATGATGCTGATGA	3429
Qy	3326	TGAGATTGGCGTAGAGCTGTGACGAAGCGGATTTGGATATTTGAAAGAAACCCTC	3381
Db	3430	CAGGATGCCCACTTACACAGCAAGAAAGACATTGATATATTCGCGGATGCCCTTC	3485

RESULT 10

ID	Accession	Standard	CDNA	5061 BP
AD	V42920	standard	CDNA	5061 BP
DI	U43920			
DI	19-OCT-1998	(first entry)		
DE	CDNA encoding a human class II PI3 kinase-C2alpha.			
DE	Human; class II phosphoinositide lipid kinase; PI3 kinase;			
OS	PI3-C2alpha; class II; resistance; Wortmannin; LY294002; ss.			
KW	Homo sapiens.			
FT	Key	Location/Qualifiers		
FT	CDS	1..5061		
FT	/*tag=	a		
FT	/product=	PI3K-C2alpha		
PN	W09832864-A2.			
PD	30-JUL-1998.			
PR	27-JAN-1998; G00244.			
PR	28-JAN-1997; GB-001652.			
PI	(LUDW-) LUDWIG INST CANCER RES.			
PI	Domini J, Waterfield MD;			
DR	WPI: 98-427960/36.			
DR	P-PSDB: W70991.			
PT	New nucleic acid encoding phosphoinositide kinase 3-C2 alpha or its			
PT	fragments - useful for, e.g. treatment of tumor cells where			
PT	phenotype is associated with expression of kinase			
PS	Claim 1; Fig 1; 52pp. English.			
CC	The present sequence encodes a human class II phosphoinositide lipid			
CC	kinase due to the presence of a conserved C2 domain found in murine and			
CC	Drosophila class II PI3 kinases, its apparent lack of a p85 binding site			
CC	and a substrate affinity to inositol lipids PtdIns and PtdIns(4)P. The			
CC	protein has resistance to PI3 kinase inhibitors Wortmannin and LY294002.			
CC	Antibodies against the protein (optionally humanised), are used to			
CC	identify class II PI3 kinases. Antisense sequences, antibodies or			
CC	dominant negative mutants of the PI3-C2alpha protein, are useful in human			
CC	or veterinary medicine to block class II kinases. They can be used to			
CC	treat tumour cells where the phenotype is associated with expression of			
CC	PI3-C2alpha protein.			
SO	Sequence	5061 BP;	1634 A;	991 C; 1002 G; 1434 T;

Query Match	2.0%	Score 68.6;	DB 1;	Length 5061;
Best Local Similarity	51.9%;	Pred. No. 3.2e-10;		
Matches 179;	Conservative 0;	Mismatches 164;	Indels 2;	Gaps 1;

ID	Accession	Standard	CDNA	5061 BP
QY	2865	GATTGGGAACCATGCGGATGTGAGATGCAAAAGCAAAAGCAAAAGCACTTACGAA	2924	
DB	3565	GCTTCGATACCTCCTGAGGAAAATCCAAAGTGATATGTGTACAGGATCCTTTAAAGAT	3624	
QY	2925	AATTCGCATCGCAAAAGAAAGATGATTAATCACTCAACGCATGAAGAATATTTTGAAGTGT	2984	

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OM nucleic - nucleic search, using sw model

Run on: July 16, 1999, 19:59:27 ; Search time 998.62 Seconds

(without alignments)
12553.051 Million cell updates/sec

Title: US-08-908-453-2

Perfect score: 3504
Sequence: 1 CGGAAGCCATGAGCTCGAG.....ACGACATCAACACTACTGCA 3504

Scoring table: IDENTITY_NUC

Searched: 808301 seqs, 1786773984 residues

Database :

GenEmbl: *
1: gb_ba1: *
2: gb_ba2: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl1: *
9: gb_pl2: *
10: gb_pr1: *
11: gb_pr2: *
12: gb_pr3: *
13: gb_ro: *
14: gb_st: *
15: gb_sy: *
16: gb_un: *
17: gb_vl: *
18: gb_hlg: *
19: em_da: *
20: em_fun: *
21: em_hum2: *
22: em_hum1: *
23: em_in: *
24: em_om: *
25: em_or: *
26: em_ov: *
27: em_pat: *
28: em_ph: *
29: em_pl: *
30: em_ro: *
31: em_sy: *
32: em_un: *
33: em_vl: *
34: em_hlg: *
35: em_st: *
36: gb_ba1: *
37: gb_ba2: *
38: gb_sts: *
39: gb_pl1: *
40: gb_pl2: *
41: gb_pr1: *
42: gb_pr2: *
43: gb_pr3: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query #
No. Match Length DB ID Description

1	3504	100.0	3504	3	CEUS6101	US6101 Caenorhabd
2	564.6	16.1	304173	18	CER622F	ALU23633 Caenorhab
3	148	4.2	3498	6	A37232	A37232 Sequence 1
4	146.4	4.2	3207	4	BOVPHOS3KN	M93252 Bovine phop
5	139.4	4.0	41812	3	CER0334	Z66519 Caenorhabd
6	130.2	3.7	3452	5	AF001076	AF001076 Gallus ga
7	130	3.7	3424	10	HSPH13K	Z28090 H.sapiens m
8	130	3.7	3424	11	HSPH13K	Z28090 H.sapiens m
9	128.6	3.7	3389	17	AF001075	AF001075 Avian sar
10	126.8	3.6	3207	10	HSU79143	U79143 Human phosp
11	126.8	3.6	3207	41	HSU79143	U79143 Human phosp
12	120.8	3.4	3207	13	MMU03279	U03279 Mus musculu
13	120.8	3.4	3132	13	MMU08587	U08587 Mus musculu
14	103.6	3.0	3668	11	HSP110DEL	Y10055 H.sapiens m
15	103.6	3.0	5220	11	HSU86453	U86453 Human phosp
16	103.6	3.0	3868	42	HSP110DEL	Y10055 H.sapiens m
17	103.6	3.0	5220	42	HSU86453	U86453 Human phosp
18	100.4	2.9	3525	11	HSU57843	U57843 Human phosp
19	100.4	2.9	3525	42	HSU57843	U57843 Human phosp
20	97.8	2.8	3213	13	RNO012482	AJ012482 Rattus no
21	96.4	2.8	3808	4	SSP120	Y10743 S.scrofa mr
22	95.6	2.7	3213	10	S67334	S67334 phosphatidy
23	95.6	2.7	3213	41	S67334	S67334 phosphatidy
24	92.4	2.6	3712	3	DMPHOS3KI	Y09070 D.melanog
25	90.2	2.6	4713	3	DDU23476	U23476 Dictyostell
26	90	2.6	5397	10	HSIDEM	X83368 H.sapiens m
27	90	2.6	5397	41	HSIDEM	X83368 H.sapiens m
28	86.8	2.5	4134	6	A50263	A50263 Sequence 1
29	86.8	2.5	4137	6	A50265	A50265 Sequence 3
30	80.8	2.3	5577	3	DDU23477	U23477 Dictyostell
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32	74.2	2.1	6358	13	ABO08791	ABO08791 Mus muscu
33	74.2	2.1	3607	13	ABO08792	ABO08792 Mus muscu
34	70.8	2.0	4880	11	HSC2P13KI	AJ000008 Homo sapi
35	70.8	2.0	4880	42	HSC2P13KI	AJ000008 Homo sapi
36	69	2.0	7654	11	HSC2P13K	Y11312 H.sapiens m
37	69	2.0	7654	42	HSC2P13K	Y11312 H.sapiens m
38	68.6	2.0	5061	11	HSPHOS13K	Y11367 H.sapiens m
39	68.6	2.0	5061	42	HSPHOS13K	Y11367 H.sapiens m
40	67.8	1.9	4758	3	DDU23478	U23478 Dictyostell
41	67.4	1.9	5296	12	HSP13KINA	Y13892 Homo sapien
42	67.4	1.9	5296	43	HSP13KINA	Y13892 Homo sapien
43	65.6	1.9	5285	13	MMU052193	U52193 Mus musculu
44	65	1.9	5067	13	MMU052193	U52193 Mus musculu
45	59.8	1.7	13862	3	CER3981	Z69660 Caenorhabd

ALIGNMENTS

RESULT 1
CEUS6101 3504 bp mRNA INV 26-FEB-1997
LOCUS Caenorhabditis elegans AGE-1 mRNA, partial cds.
DEFINITION
ACCESSION U56101
NID 91850328
KEYWORDS
SOURCE
ORGANISM

Caenorhabditis elegans.
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabdillia; Rhabdillia; Rhabdillia; Rhabdillia;
Rhabdillidae; Pelodierinae; Caenorhabditis.
REFERENCE
AUTHORS Morris J.Z., Tissenbaum H.A. and Ruvkun, G.
TITLE A phosphatidylinositol-3-OH kinase family member regulating
longevity and diapause in Caenorhabditis elegans
JOURNAL Nature 382 (6591), 536-539 (1996)
MEDLINE 96320556
REFERENCE 2 (bases 1 to 3504)

REFERENCE
AUTHORS Morris J.Z., Tissenbaum H.A. and Ruvkun, G.B.
TITLE Direct Submission
JOURNAL Submitted (22-APR-1996) Mol. Biol., Mass General Hospital, Wellman
8, Boston, MA 02114, USA

REFERENCE 3 (bases 1 to 3504)
 AUTHORS Morris, J. Z., Tissenbaum, H. A. and Ruvkun, G. B.
 TITLE Direct Submission
 JOURNAL Submitted (24-FEB-1997) Mol. Biol., Mass General Hospital, Wellman
 8, Boston, MA 02114, USA
 REMARK Sequence and protein updated by submitter
 COMMENT On Feb 26, 1997 this sequence version replaced gi:1778714.
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 /strain="N2"
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CDS

BASE COUNT 1069 a 688 c 826 g 921 t
 ORIGIN

Query Match 100.0%; Score 3504; DB 3; Length 3504;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 241 TGGTTCTTGCAGAAATGGAGACATCGTAGAAATCAACATCAATTTCACAACTCA 300
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 241 TGGTTCTTGCAGAAATGGAGACATCGTAGAAATCAACATCAATTTCACAACTCA 300
 241 TGGTTCTTGCAGAAATGGAGACATCGTAGAAATCAACATCAATTTCACAACTCA 300
 301 CTTTTCGAAATGATGCTCGATGAGAGTGGGACATATTCGCGTAAGCCACGAGATTAT 360
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 301 CTTTTCGAAATGATGCTCGATGAGAGTGGGACATATTCGCGTAAGCCACGAGATTAT 360
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 361 GTGTCACAGACATGTAATATTTGGCGAAATTTGAAGTTATATTACAGACATCAACC 420

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 421 CTTGGAATTTAGCTCCAGCGCACTTTCCCAATGCTTTTCTTACCAACCTGATGA 480
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 421 CTTGGAATTTAGCTCCAGCGCACTTTCCCAATGCTTTTCTTACCAACCTGATGA 480
 421 CTTGGAATTTAGCTCCAGCGCACTTTCCCAATGCTTTTCTTACCAACCTGATGA 480
 481 ATTAACAGGATTAAGAAATTAATGATGATATTAATGATGATGATGATGATGATGAT 540
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RESULT 2
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LOCUS Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from
DEFINITION clone y62F5; HGVS phase 1.
ACCESSION AL023633
NID 93970663

Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favell, J., Fulton, L., Gardner, A., Green, P., Harkin, T., Hillier, L., Jeter, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Riffen, L., Roopra, A., Saunders, D., Showkeen, R., Smalton, N., Smith, A., Sonhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkinson-Sprat, J., and Woldman, P.

2. 2 kb of contiguous nucleotide sequence from chromosome III of *C. elegans*

JOURNAL Nature 368 (6466), 32-38 (1994)

MEDLINE 94150718

REFERENCE 2 (bases 1 to 41812)

AUTHORS Swaburne, J.

TITLE Direct Submission

JOURNAL Submitted (27-OCT-1995) Louis, MO 63110, USA. E-mail: jesusanger.ac.uk or rwenematode.wustl.edu

COMMENT Coding sequences below are predicted from computer analysis, using predictions from GeneFinder (P. Green, U. Washington), and other available information.

For a graphical representation of this sequence and its analysis see: -

http://webace.sanger.ac.uk/cgi-bin/displayrb-wormaceclass-Sequence object-B0334

Current sequence finishing criteria for the *C. elegans* genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

This sequence is the entire insert of clone B0334. The true right end of clone W02B12 is at 4181 in this sequence. The start of this sequence (1..104) overlaps with the end of sequence Z65521.

Location/Qualifiers

1. 41812

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/db_xref="taxon:6239"

/chromosome="II"

/clone="B0334"

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complement(join(4176..4394,4819..4966,5021..5163,5218..5529,5685..5735))

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/note="similar to potassium channel protein; cDNA EST EMBL:D70075 comes from this gene; cDNA EST EMBL:D66354 comes from this gene"

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/note="similar to Transthyretin-like family; cDNA EST EMBL:D66717 comes from this gene"

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complement(join(10596..11180,11230..12189,12420..12524,12857..13062,13803..13851))

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/note="similar to oxalyl-CoA decarboxylase; cDNA EST EMBL:D71591 comes from this gene; cDNA EST EMBL:D66565 comes from this gene; cDNA EST EMBL:D7312 comes from this gene; cDNA EST EMBL:D70388 comes from this gene; cDNA EST EMBL:D74248 comes from this gene; cDNA EST EMBL:D68660 comes from this gene; cDNA EST EMBL:D76344 comes from this gene; cDNA EST EMBL:D35993 comes from this gene; cDNA EST EMBL:C11330 comes from this gene; cDNA EST EMBL:C13447 comes from this gene; cDNA EST EMBL:C1140 comes from this gene; cDNA EST EMBL:C13141 comes from this gene; cDNA EST EMBL:C12333 comes from this gene"

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/note="similar to Thiamine pyrophosphate enzymes; cDNA EST EMBL:D36315 comes from this gene; cDNA EST EMBL:D33464 comes from this gene"

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/gene="B0334.11"

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/gene="B0334.11"

/note="cDNA EST yk52496.5 comes from this gene; cDNA EST

FEATURES BBT, UK Location/Qualifiers
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BASE COUNT 1134 a 618 c 709 g 963 t

ORIGIN

Query Match 3.7%; Score 130; DB 10; Length 3424;
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Matches 719; Conservative 0; Mismatches 765; Indels 90; Gaps 4;

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RESULT 8
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ACCESSION 229090
KEYWORDS 9472990
SOURCE phosphatidylinositol 3-kinase.
ORGANISM human.
Eukaryote; mitochondria; eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1068)
Volinia, S., Hiles, I., Ormondey, E., Nizetic, D., Antonacci, R.,
Rocchi, M. and Waterfield, M.D.
Molecular cloning, cDNA sequence, and chromosomal localization of
the human phosphatidylinositol 3-kinase p110 alpha (PIK3CA) gene
Genomics 24 (3), 472-477 (1994)
JOURNAL 952916
REFERENCE 2 (bases 1 to 3424)
Volinia, S.
Direct Submission
TITLE Submitted (16-DEC-1993) Stefano Volinia, Receptor Studies, Ludwig
Institute for Cancer Research, 91 Riding House Street, London, W1P
8BT, UK
FEATURES
source 1. Location/Qualifiers
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BASE COUNT 1134 a 618 c 709 g 963 t
ORIGIN

Query Match 3.7%; Score 130; DB 41; Length 3424;
Best Local Similarity 45.7%; Pred. No. 5, 3e-23;
Matches 719; Conservative 0; Mismatches 765; Indels 90; Gaps 4;

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Dd	3013	CTTTCTCAATGATGCTGTGGCTCTGGAATGCCAGAACTACAATCTTTTGATGACATTGCA	3072
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DEFINITION	Avian sarcoma virus 16 gag-v-phosphoinositide 3-kinase catalytic subunit fusion protein (gag-v-p3k) and retroviral env mRNAs, partial cds.		
ACCESSION	AF001075		
NID	92245502		
KEYWORDS			
SOURCE	Avian sarcoma virus 16.		
ORGANISM	Avian sarcoma virus 16.		
REFERENCE	Viruses; Retrovid viruses; Retroviridae; Avian type C retroviruses. 1 (bases 1 to 3389)		
AUTHORS	Chang,H.W., Aoki,M., Furman,D., Auger,K.R., Bellacosa,A., Tsichlis,P.N., Cantley,L.C., Roberts,T.M. and Vogt,P.K.		
TITLE	Transformation of chicken cells by the gene encoding the catalytic subunit of p13-kinase		
JOURNAL	Science 276 (5320), 1848-1850 (1997)		
MEDLINE	97334438		
REFERENCE	2 (bases 1 to 3389)		
AUTHORS	Chang,H.W., Aoki,M. and Vogt,P.K.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-APR-1997) Molecular & Experimental Medicine, The Scripps Research Institute, 10550 N. Torrey Pines Road, Mail-drop BCC-239, La Jolla, CA 92037, USA		
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misc_feature			

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RESULT	11
LOCUS	HSU79143
DEFINITION	Human phosphoinositide 3'-hydroxylase p110-alpha subunit mRNA,
ACCESSION	U79143
NID	g1763625
KEYWORDS	
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	Stirdiavantz,S.M., Ahern,J., Conroy,R.R., Barnett,S.F., Ledder,L.M.

TITLE	Catalytic Activity of the p110-alpha Subunit of Human Phosphoinositide 3'-Hydroxyltransferase Is Required for Signal Transduction
JOURNAL	Bioorg. Med. Chem. (1996) In press
REFERENCE	2 (bases 1 to 3207)
AUTHORS	Stridh, V., S.M., Ahern, J., Conroy, R.R., Barnett, S.F., Iedder, L.M., Oliff, A. and Heimbach, D.C.
TITLE	Direct Submission
JOURNAL	Submitted (21-NOV-1996) Cancer Research, Merck Research Labs, Sunningtown Pike, West Point, PA 19486, USA
FEATURES	location/Qualifiers
SOURCE	1. 3207

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ORIGIN

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Query Match	3.6%	Score 126.8;	DB 41;	Length 3207;
Best Local Similarity	45.6%;	Pred. No 3.5e-32;		
Matches 717;	Conservative 0;	Mismatches 767;	Indels 90;	Gaps 4

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RESULT 12

MMU03279

LOCUS

DEFINITION

ACCESSION

U03279

KEYWORDS

NID

ORGANISM

house mouse.

Mus musculus

Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 3207)

AUTHORS

Klippel, A., Escobedo, J.A., Hirano, M. and Williams, L.T.

TITLE

The interaction of small domains between the subunits of phosphatidylinositol 3-kinase determines enzyme activity

Mol. Cell. Biol. 14, 2675-2685 (1994)

JOURNAL

94187738

MEDLINE

2 (bases 1 to 3207)

REFERENCE

Klippel-Giese, A.

AUTHORS

Direct Submission

Submitted (05-NOV-1993) Anke Klippel-Giese, CVRI and Dalich Research Center, University of California San Francisco, 505 Parnassus Ave, Long Hospital, San Francisco, CA 94143, USA

JOURNAL

Location/Qualifiers

1. 3207

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1. 3207

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BASE COUNT

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ORIGIN

Query Match 3.48; Score 120.8; DB 13; Length 3207;
 Best Local Similarity 53.08; Pred. No. 1.1e-20;
 Matches 282; Conservative 0; Mismatches 247; Indels 3; Gaps 1;

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DEFINITION	MMU86587	3132 bp	mRNA
LOCATION			07-JUL-1998
ACCESSION			Mus musculus phosphatidylinositol 3-kinase catalytic subunit p110
NID	U86587		delta mRNA, complete cds.
KEYWORDS	g2331237		
SOURCE			house mouse.
ORGANISM			Mus musculus
REFERENCE			Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
AUTHORS			Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
TITLE			Murinae; Mus.
			1 (bases 1 to 3132)
			Chanity,D., Vojtek,A., Kashishian,A., Holtzman,D.A., Wood,C.,
			Gray,P.W., Cooper,J.A. and Hoekstra,M.F.
			p110delta, a novel phosphatidylinositol 3-kinase catalytic subunit
			that associates with p85 and is expressed predominantly in
			leukocytes
JOURNAL	J Biol. Chem.	272 (31),	19236-19241 (1997)
MEDLINE			
REFERENCE	97382246		
AUTHORS			2 (bases 1 to 3132)
TITLE			Vojtek,A.B. and Cooper,J.
JOURNAL			Direct Submission
			Submitted (22-JAN-1997) Biological Chemistry, University of
			Michigan, 3323 MSB III, Box 0636, Ann Arbor, MI 48109-0636, USA
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Db 3083 CCAAAAGCACTGCTGGCGGCACATGT 3110		

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ORIGIN

Query Match 3.0%: Score 106.8; DB 13; Length 3132;

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Matches 272; Conservative 0; Mismatches 227; Indels 9; Gaps 2;

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RESULT 14

HSP110DEL HSP110DEL 3868 bp RNA PRI 16-MAY-1997

LOCUS H.sapiens mRNA for phosphoinositide 3-kinase.

DEFINITION Y10055

ACCESSION g2104839

NID

KEYWORDS p110delta; phosphoinositide 3-kinase.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE	1 (bases 1 to 3868)	
AUTHORS	Vanhaesebroeck, B., Welham, M.J., Kotani, K., Stein, R., Warne, P.H., Zvelebil, M.J., Higashi, K., Vollmar, S., Downward, J. and Waterfield, M.D.	
TITLE	p110delta, a novel phosphoinositide 3-kinase in leukocytes	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 94 (1997), 4330-4335 (1997)	
REFERENCE	2 (bases 1 to 3868)	
AUTHORS	Vanhaesebroeck, B.A.M.	
TITLE	Direct Submission	
JOURNAL	Submitted (13-DEC-1996) B.A.M. Vanhaesebroeck, Ludwig Institute for Cancer Research, UCL/Middlesex Hospital Branch, 91 Riding House Street, London N3 2EU, UK	
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